

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 14, 2006, 21:02:04 ; Search time 46 Seconds
(without alignments)
938.189 Million cell updates/sec

Title: US-09-927-458-2
Perfect score: 2754
Sequence: 1 MRLRVLRLKRTWPLEVTE.....DRPFPRSPGRPTDGRLSFM 522

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCUS_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2748	99.8	557	2	US-09-949-016-10867
2	2744	99.6	522	2	US-09-591-694-10
3	2489	90.4	482	2	US-09-385-219A-14
4	2270	82.4	443	2	US-09-591-694-8
5	553	20.1	102	2	US-09-621-976-5935
6	194	7.0	39	2	US-09-385-219A-21
7	189	6.9	38	2	US-09-172-841-47
8	189	6.9	38	2	US-09-951-621-47
9	164	6.0	38	2	US-09-172-841-49
10	164	6.0	38	2	US-09-951-621-49
11	144	5.2	321	2	US-09-166-350-15
12	139	5.0	327	2	US-09-591-694-12
13	139	5.0	327	2	US-09-385-219A-58
14	117.5	4.3	503	2	US-09-599-287A-2
15	117.5	4.3	503	2	US-10-078-547-2
16	117	4.2	507	2	US-09-599-287A-24
17	117	4.2	507	2	US-10-078-547-24
18	112	4.1	690	2	US-09-248-796A-19169
19	111.5	4.0	506	2	US-09-949-016-11282
20	111.5	4.0	955	2	US-09-949-016-8369
21	111	4.0	406	2	US-10-104-047-3010
22	110.5	4.0	553	2	US-09-949-016-7961
23	110	4.0	424	2	US-09-538-092-1338
24	109	4.0	3730	2	US-09-949-016-9908
25	107.5	3.9	776	2	US-09-252-991A-28446
26	107	3.9	78	1	US-08-487-359-5
27	107	3.9	78	1	US-08-222-798A-5

28	107	3.9	489	2	US-09-543-681A-7388	Sequence 7388, Ap
29	107	3.9	557	2	US-09-949-016-7621	Sequence 7621, Ap
30	105	3.8	297	2	US-09-252-991A-29217	Sequence 29217, A
31	105	3.8	502	2	US-09-839-577A-14	Sequence 14, Appl
32	105	3.8	662	2	US-09-949-016-3186	Sequence 9186, Ap
33	105	3.8	1031	2	US-10-104-047-2327	Sequence 2327, Ap
34	104.5	3.8	850	2	US-09-949-016-11324	Sequence 11324, A
35	104	3.8	1312	2	US-09-554-572-26	Sequence 26, Appl
36	103.5	3.8	79	1	US-08-487-359-8	Sequence 8, Appl
37	103.5	3.8	79	1	US-08-222-798A-8	Sequence 8, Appl
38	103.5	3.8	580	2	US-08-966-865-1	Sequence 1, Appl
39	103.5	3.8	580	2	US-09-129-668-1	Sequence 1, Appl
40	103.5	3.8	888	1	US-08-861-464-6	Sequence 6, Appl
41	103.5	3.8	888	1	US-08-396-001-6	Sequence 6, Appl
42	103.5	3.8	888	2	US-09-323-433A-6	Sequence 6, Appl
43	103.5	3.8	888	2	US-09-826-752-6	Sequence 6, Appl
44	103	3.7	133	2	US-09-252-991A-21490	Sequence 21490, A
45	103	3.7	431	2	US-09-248-796A-17260	Sequence 17260, A

ALIGNMENTS

RESULT 1
US-09-949-016-10867
; Sequence 10867, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTIER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10867
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10867

Query Match	99.8%	Score	2748	DB	2	Length	557
Best Local Similarity	99.8%	Pred. No.	2.2e-255				
Matches	521	Conservative	0	Mismatches	1	Indels	0
Gap	0						
Qy	1	MRLRVLRLKRTWPLEVTEPTTGHRLSHRLSLCTWGYSSNTRFTITLNYKDPPLTGDE	60				
Db	36	MRLRVLRLKRTWPLEVTEPTTGHRLSHRLSLCTWGYSSNTRFTITLNYKDPPLTGDE	95				
Qy	61	ETLASGIVSGDILICILQDDIPAPNIPSTDSHSLQNEQPSLATSSNOTSMQDEQP	120				
Db	96	ETLASGIVSGDILICILQDDIPAPNIPSTDSHSLQNEQPSLATSSNOTSMQDEQP	155				
Qy	121	SDSFQQAAGSGVWDDSLGPGSQNFAESIQNAHMAEGTGFYPSPEMLCSESVGEQVP	180				
Db	156	SDSFQQAAGSGVWDDSLGPGSQNFAESIQNAHMAEGTGFYPSPEMLCSESVGEQVP	215				
Qy	181	HSLETLYQSADCSANDALIVLIHLLMESGYIPQGTAKALSMPKRWKLSGVYKLYQMH	240				
Db	216	HSLETLYQSADCSANDALIVLIHLLMESGYIPQGTAKALSMPKRWKLSGVYKLYQMH	275				
Qy	241	PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKELGENVANYKD	300				
Db	276	PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKELGENVANYKD	335				
Qy	301	LQKLSRLFKDQLVYVPLIAFTFQALNLPDVFGLVPLLEKLRIFRLLDVRSLVSLSAVCR	360				


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RESULT 4
US-09-591-694-8
; Sequence 8, Application US/09591694
; Patent No. 6638734
; GENERAL INFORMATION:
; APPLICANT: John C. Reed
; APPLICANT: Shu-ichi Matsuzawa
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; FILE OF INVENTION: in Protein Degradation, Products and Methods Related Thereto
; FILE REFERENCE: P-LJ 4220
; CURRENT APPLICATION NUMBER: US/09/591,694
; CURRENT FILING DATE: 2000-06-09
; EARLIER APPLICATION NUMBER: US 09/330,517
; EARLIER FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-591-694-8

Query Match      82.4%; Score 2270; DB 2; Length 443;
Best Local Similarity 99.8%; Pred. No. 1.5e-209; Indels 0; Gaps 0;
Matches 430; Conservative 1; Mismatches 0;

Qy 92 DSEHSSLQNNQPSLATSSNQTSMDQPSDSFGQAAQSGVWDDSMGLGPSQNFAEESI 151
Db 13 DSEHSSLQNNQPSLATSSNQTSMDQPSDSFGQAAQSGVWDDSMGLGPSQNFAEESI 72

Qy 152 QDNHMAEGTGTFYSEPMLCSESVEGVPHSLETLYQSADCSNDALIVLIHLLMLES 211
Db 73 QDNHMAEGTGTFYSEPMLCSESVEGVPHSLETLYQSADCSNDALIVLIHLLMLES 132

Qy 212 YIPGTTAKALSMPEKKWLSGVYKLYMHPLCEGSSATLTCVPLGNLIVVNATLKINNEI 271
Db 133 YIPGTTAKALSMPEKKWLSGVYKLYMHPLCEGSSATLTCVPLGNLIVVNATLKINNEI 192

Qy 272 RSVKRLQLLPESFICEKKEKLGENVANIYKDLQKLSRLFKDLVYPLLAFTQALNLPDVF 331
Db 193 RSVKRLQLLPESFICEKKEKLGENVANIYKDLQKLSRLFKDLVYPLLAFTQALNLPDVF 252

Qy 332 LVLPLELKLIRIFRLLDVRSVLSAVCRDLFTASNDPLLRFLYLRDRDNTVRVQD 391
Db 253 LVLPLELKLIRIFRLLDVRSVLSAVCRDLFTASNDPLLRFLYLRDRDNTVRVQD 312

Qy 392 WKELYRKRHIQRKESPKGRFVMLLPSSHTTTPFYPNPLHRRPPSSRLPGIIGGEYD 451
Db 313 WKELYRKRHIQRKESPKGRFVMLLPSSHTTTPFYPNPLHRRPPSSRLPGIIGGEYD 372

Qy 452 PTLPYVGDPISLIPGGETPSQFPPLRPDPVGPPLPGNPILPGRGGPNDRPFPSPR 511
Db 373 PTLPYVGDPISLIPGGETPSQFPPLRPDPVGPPLPGNPILPGRGGPNDRPFPSPR 432

Qy 512 GRPTDGRLSFM 522
Db 433 GRPTDGRLSFM 443

RESULT 5
US-09-621-976-5935
; Sequence 5935, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm

Query Match      82.4%; Score 2270; DB 2; Length 443;
Best Local Similarity 99.8%; Pred. No. 1.5e-209; Indels 0; Gaps 0;
Matches 430; Conservative 1; Mismatches 0;

Qy 92 DSEHSSLQNNQPSLATSSNQTSMDQPSDSFGQAAQSGVWDDSMGLGPSQNFAEESI 151
Db 13 DSEHSSLQNNQPSLATSSNQTSMDQPSDSFGQAAQSGVWDDSMGLGPSQNFAEESI 72

Qy 152 QDNHMAEGTGTFYSEPMLCSESVEGVPHSLETLYQSADCSNDALIVLIHLLMLES 211
Db 73 QDNHMAEGTGTFYSEPMLCSESVEGVPHSLETLYQSADCSNDALIVLIHLLMLES 132

Qy 212 YIPGTTAKALSMPEKKWLSGVYKLYMHPLCEGSSATLTCVPLGNLIVVNATLKINNEI 271
Db 133 YIPGTTAKALSMPEKKWLSGVYKLYMHPLCEGSSATLTCVPLGNLIVVNATLKINNEI 192

Qy 272 RSVKRLQLLPESFICEKKEKLGENVANIYKDLQKLSRLFKDLVYPLLAFTQALNLPDVF 331
Db 193 RSVKRLQLLPESFICEKKEKLGENVANIYKDLQKLSRLFKDLVYPLLAFTQALNLPDVF 252

Qy 332 LVLPLELKLIRIFRLLDVRSVLSAVCRDLFTASNDPLLRFLYLRDRDNTVRVQD 391
Db 253 LVLPLELKLIRIFRLLDVRSVLSAVCRDLFTASNDPLLRFLYLRDRDNTVRVQD 312

Qy 392 WKELYRKRHIQRKESPKGRFVMLLPSSHTTTPFYPNPLHRRPPSSRLPGIIGGEYD 451
Db 313 WKELYRKRHIQRKESPKGRFVMLLPSSHTTTPFYPNPLHRRPPSSRLPGIIGGEYD 372

Qy 452 PTLPYVGDPISLIPGGETPSQFPPLRPDPVGPPLPGNPILPGRGGPNDRPFPSPR 511
Db 373 PTLPYVGDPISLIPGGETPSQFPPLRPDPVGPPLPGNPILPGRGGPNDRPFPSPR 432

Qy 512 GRPTDGRLSFM 522
Db 433 GRPTDGRLSFM 443
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; SEQ ID NO 5935.
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 87
; OTHER INFORMATION: Xaa = Cys,Gly
US-09-621-976-5935

Query Match      20.1%; Score 553; DB 2; Length 102;
Best Local Similarity 99.0%; Pred. No. 2.4e-45; Indels 0; Gaps 0;
Matches 98; Conservative 0; Mismatches 1;

Qy 413 MLLPSSHTTTPFYFNPLHRRPPSSRLPGIIGGEYDQRTLPYVGDPISLIPGGETP 472
Db 1 MLLPSSHTTTPFYFNPLHRRPPSSRLPGIIGGEYDQRTLPYVGDPISLIPGGETP 60

Qy 473 SQFPPLRPDPVGPPLPGNPILPGRGGPNDRPFPSPR 511
Db 61 SQFPPLRPDPVGPPLPGNPILPGRGGPNDRPFPSPR 99

RESULT 6
US-09-385-219A-21
; Sequence 21, Application US/09385219A
; Patent No. 6720181
; GENERAL INFORMATION:
; APPLICANT: Chiaux, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/09/385,219A
; CURRENT FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-385-219A-21

Query Match      7.0%; Score 194; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.8e-11; Indels 0; Gaps 0;
Matches 39; Conservative 0; Mismatches 0;

Qy 335 LPLELKLIRIFRLLDVRSVLSAVCRDLFTASNDPLLR 373
Db 1 LPLELKLIRIFRLLDVRSVLSAVCRDLFTASNDPLLR 39

RESULT 7
US-09-172-841-47
; Sequence 47, Application US/09172841
; Patent No. 6232081
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeffrey W.
; APPLICANT: Elledge, Stephen J.
; TITLE OF INVENTION: F-BOX PROTEINS AND GENES
; FILE REFERENCE: BCM-03510
; CURRENT APPLICATION NUMBER: US/09/172,841
; CURRENT FILING DATE: 1998-10-15
; EARLIER APPLICATION NUMBER: 08/951,621
; EARLIER FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 47
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-172-841-47

Query Match          6.9%; Score 189; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 5.2e-11;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 335 LPLEKLRIFRLDVRVSLSAVCRDLFTASNDPLW 372
      |||
Db 1 LPLEKLRIFRLDVRVSLSAVCRDLFTASNDPLW 38

RESULT 8
US-08-951-621-47
; Sequence 47, Application US/08951621
; Patent No. 6573094
; GENERAL INFORMATION:
; APPLICANT: HARPER, JEFFREY W.
; APPLICANT: ELLEDGE, STEPHEN J.
; TITLE OF INVENTION: F-BOX GENES AND PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,621
; FILING DATE: 16-OCT-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: BCM-02999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
US-08-951-621-47

Query Match          6.9%; Score 189; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 5.2e-11;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 335 LPLEKLRIFRLDVRVSLSAVCRDLFTASNDPLW 372
      |||
Db 1 LPLEKLRIFRLDVRVSLSAVCRDLFTASNDPLW 38

RESULT 9
US-09-172-841-49
; Sequence 49, Application US/09172841
; Patent No. 6232081
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeffrey W.
; APPLICANT: Elledge, Stephen J.
; TITLE OF INVENTION: F-BOX PROTEINS AND GENES
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; FILE REFERENCE: BCM-03510
; CURRENT APPLICATION NUMBER: US/09/172,841
; CURRENT FILING DATE: 1998-10-15
; EARLIER APPLICATION NUMBER: 08/951,621
; EARLIER FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-172-841-49

Query Match          6.0%; Score 164; DB 2; Length 38;
Best Local Similarity 86.8%; Pred. No. 1.3e-08;
Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 335 LPLEKLRIFRLDVRVSLSAVCRDLFTASNDPLW 372
      |||
Db 1 LPLEKLRIFRLDVRVSLSAVCHDLLIASNDPLW 38

RESULT 10
US-08-951-621-49
; Sequence 49, Application US/08951621
; Patent No. 6573094
; GENERAL INFORMATION:
; APPLICANT: HARPER, JEFFREY W.
; APPLICANT: ELLEDGE, STEPHEN J.
; TITLE OF INVENTION: F-BOX GENES AND PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,621
; FILING DATE: 16-OCT-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: BCM-02999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
US-08-951-621-49

Query Match          6.0%; Score 164; DB 2; Length 38;
Best Local Similarity 86.8%; Pred. No. 1.3e-08;
Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 335 LPLEKLRIFRLDVRVSLSAVCRDLFTASNDPLW 372
      |||
Db 1 LPLEKLRIFRLDVRVSLSAVCHDLLIASNDPLW 38

RESULT 11
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; Sequence 2, Application US/09599287A
; Patent No. 6635446
; GENERAL INFORMATION:
; APPLICANT: Narayanaswamy Ramesh
; APPLICANT: Ines M. Anton
; APPLICANT: John H. Hartwig
; APPLICANT: Raif S. Gena
; TITLE OF INVENTION: WIP, A WASP-Associated Protein
; FILE REFERENCE: 1242.1022-004
; CURRENT APPLICATION NUMBER: US/09/599,287A
; CURRENT FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: PCT/US98/27501
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/101,457
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/068,533
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Human
US-09-599-287A-2

Query Match 4.3%; Score 117.5; DB 2; Length 503;
Best Local Similarity 33.1%; Pred. No. 0.028; 41; Indels 43; Gaps 9;
Matches 46; Conservative 9; Mismatches 41; Indels 43; Gaps 9;

Qy 415 LPSSTHTIPFPYNPLHPPPPSSR-----LPPGIIGGEYDQRTLPYVGDPISSL---IP 466
Db 294 VPSTPR--PSAPHRPHLRPPPSRPGPPPLPPSSSGN--DETFLPQRNLSSLSTPPLP 349
Qy 467 GPGET-----PSQFPPLRPRFDP--VGPLPGNPPI-----LPG----- 497
Db 350 SPGRSGPLPPPSERPPPPVDPDPPGRSGPLPPPPVSRNGSTSRALPATQLPSRSGVDS 409
Qy 498 -RGGNDRF-PFRPSRGRP 514
Db 410 PRSGRPLPPDRPSAGAP 428

RESULT 15
US-10-078-547-2
; Sequence 2, Application US/10078547
; Patent No. 6927318
; GENERAL INFORMATION:
; APPLICANT: Narayanaswamy Ramesh
; APPLICANT: Miguel A. de la Fuente
; APPLICANT: Ines M. Anton
; APPLICANT: Raif S. Gena
; TITLE OF INVENTION: WIP, A WASP-Associated Protein
; FILE REFERENCE: 1242.1022-005
; CURRENT APPLICATION NUMBER: US/10/078,547
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/599,287
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: PCT/US98/27501
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/101,457
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/068,533
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Human
US-10-078-547-2

Query Match 4.3%; Score 117.5; DB 2; Length 503;
Best Local Similarity 33.1%; Pred. No. 0.028;

Matches 46; Conservative 9; Mismatches 41; Indels 43; Gaps 9;

Qy 415 LPSSTHTIPFPYNPLHPPPPSSR-----LPPGIIGGEYDQRTLPYVGDPISSL---IP 466
Db 294 VPSTPR--PSAPHRPHLRPPPSRPGPPPLPPSSSGN--DETFLPQRNLSSLSTPPLP 349
Qy 467 GPGET-----PSQFPPLRPRFDP--VGPLPGNPPI-----LPG----- 497
Db 350 SPGRSGPLPPPSERPPPPVDPDPPGRSGPLPPPPVSRNGSTSRALPATQLPSRSGVDS 409
Qy 498 -RGGNDRF-PFRPSRGRP 514
Db 410 PRSGRPLPPDRPSAGAP 428

Search completed: February 14, 2006, 21:03:23
Job time : 47 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2006, 20:54:48 ; Search time 234 Seconds
(without alignments)
1573.871 Million cell updates/sec

Title: US-09-927-458-2
Perfect score: 2754
Sequence: 1 MRLVRLKLTWPLEVETE.....DRFPFRPSRGRTDGRLSFM 522

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	2748	99.8	522	1	FBX7	HUMAN	Q9Y311 homo sapien
2	2532	91.9	528	2	Q5TGC3	HUMAN	Q5TGC3 homo sapien
3	2214	80.4	443	2	Q5RBD1	PONPY	Q5RBD1 pongo pygma
4	1984	72.0	522	2	Q68FS3	RAT	Q68FS3 rattus norv
5	1977.5	71.8	523	2	Q8K0A5	MOUSE	Q8K0A5 mus musculus
6	1295	47.0	361	2	Q6Y017	CHICK	Q6Y017 gallus gall
7	1261	45.8	399	2	Q5F421	CHICK	Q5F421 gallus gall
8	1247	45.3	233	2	Q5HYB3	HUMAN	Q5HYB3 homo sapien
9	1125	40.8	478	2	Q6DE59	XENLA	Q6DE59 xenopus lae
10	1059	38.5	472	2	Q5PQ43	XENLA	Q5PQ43 xenopus lae
11	877	31.7	486	2	Q4V8X6	BRARE	Q4V8X6 brachydanio
12	873.5	31.7	483	2	Q5SPK1	BRARE	Q5SPK1 brachydanio
13	851.5	30.9	471	2	Q4T8W7	TETNG	Q4T8W7 tetraodon n
14	240.5	8.7	475	2	Q5ZUB8	ARATH	Q5ZUB8 arabidopsis
15	205	7.4	776	2	Q8GZV6	ORISA	Q8GZV6 oryza sativ
16	187.5	6.8	350	2	Q5ZUB9	ARATH	Q5ZUB9 arabidopsis
17	181.5	6.6	1212	2	Q515H3	ENTHI	Q515H3 entamoeba h
18	157	5.7	326	2	Q4S822	DICTDI	Q4S822 dictyosteli
19	147	5.3	270	1	PSMF1	DROME	Q5V637 drosophila
20	145.5	5.3	434	2	Q4W8W0	HUMAN	Q4W8W0 homo sapien
21	145.5	5.3	554	2	Q59EH8	HUMAN	Q59EH8 homo sapien
22	144	5.2	447	1	FBX9	HUMAN	Q5UK97 homo sapien
23	143.5	5.2	271	2	Q5ZJ33	CHICK	Q5ZJ33 gallus gall
24	140	5.1	435	1	FBX9	RAT	Q5U213 rattus norv
25	138.5	5.0	356	2	Q7ZTY2	BRARE	Q7ZTY2 brachydanio
26	135	4.9	437	1	FBX9	MOUSE	Q5BK06 mus musculus
27	134.5	4.9	1183	2	Q7TSH6	MOUSE	Q7TSH6 mus musculus
28	134.5	4.9	1209	2	Q6PFQ0	MOUSE	Q6PFQ0 mus musculus
29	134	4.9	3148	2	Q8H6Q8	PONTR	Q8H6Q8 poncirus tr
30	132	4.8	405	2	Q52F83	MAGGR	Q52F83 magnaporthe
31	130.5	4.7	355	2	Q5ZHM6	CHICK	Q5ZHM6 gallus gall

32	129.5	4.7	1200	2	Q692P8_MOUSE	Q692P8 mus musculus
33	129	4.7	569	2	Q54CP0_DICTDI	Q54CP0 dictyosteli
34	129	4.7	745	2	Q6Z125_ORISA	Q6Z125 oryza sativ
35	128.5	4.7	850	2	Q17055-CAEEL	Q17055 caenorhabdi
36	127	4.6	579	2	Q4RLQ7_TETNG	Q4RLQ7 tetraodon n
37	126.5	4.6	431	2	Q7SY92_XENLA	Q7SY92 xenopus lae
38	126	4.6	355	1	FBX32_HUMAN	Q969P5 homo sapien
39	124.5	4.5	356	2	Q4RFD2_TETNG	Q4RFD2 tetraodon n
40	124.5	4.5	434	2	Q5CD94-CRYHO	Q5CD94 cryptospori
41	124.5	4.5	920	1	21MP7_HUMAN	Q8NF64 homo sapien
42	124	4.5	980	2	Q60PF6-CAEBR	Q60PF6 caenorhabdi
43	123.5	4.5	1874	2	Q5SBA7_DICTDI	Q5SBA7 dictyosteli
44	123.5	4.5	4527	2	Q4RVG0_TETNG	Q4RVG0 tetraodon n
45	123	4.5	271	1	PSMF1_HUMAN	Q92530 homo sapien

ALIGNMENTS

RESULT 1
FBX7_HUMAN
ID FBX7_HUMAN STANDARD; PRT; 522 AA.
AC Q9Y311; Q5TGC4; Q96HM6; Q9UF21; Q9UKT2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE F-box only protein 7.
GN Name=FBX07; Synonyms=FBX7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE OF 41-522, AND VARIANT ILB-115.
RX MEDLINE=20003060; PubMed=10531035; DOI=10.1016/S0960-9822(00)80020-2;
RA Cenciarelli C., Chiaur D.S., Guardavaccaro D., Parks W., Vidal M.,
Pagano M.;
RT "Identification of a family of human F-box proteins.";
RL Curr. Biol. 9:1177-1179(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=20399565; PubMed=10945468; DOI=10.1006/geno.2000.6211;
RA Ilyin G.P., Riialand M., Pigeon C., Gugen-Guillouzo C.;
RT "cDNA cloning and expression analysis of new members of the mammalian
F-box protein family.";
RL Genomics 67:40-47(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Collins J.E., Huckle E.J.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX PubMed=15461802; DOI=10.1186/gb-2004-5-10-r84;
RA Collins J.E., Wright C.E., Edwards C.A., Davis M.P., Grinham J.A.,
Cole C.G., Goward M.E., Aguado B., Malliya M., Mokrab Y., Huckle E.J.,
Beare D.M., Dunham I.;
RT "A genome annotation-driven approach to cloning the human ORFeome.";
RL Genome Biol. 5:RESEARCH84.1-RESEARCH84.11(2004).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,
Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
Begguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
Gilbert J.G.R., Goward M.B., Grahame D.V., Griffiths M.N.D., Hall C.,
Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,

RESULT 2
QSTGC3_HUMAN
ID QSTGC3_HUMAN PRELIMINARY; PRT; 528 AA.
AC QSTGC3;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE F-box protein 7 (Fragment).
GN Name=FBX07; ORFNames=LL22NC03-28H9.2-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RS Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RA Davies J.;
RP NUCLEOTIDE SEQUENCE.
RS Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RA Smith M.;
RP NUCLEOTIDE SEQUENCE.
RS Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RA EMBL; AL035068; CAI19334.1; -; Genomic DNA.
DR EMBL; Z71183; CAI18783.1; -; Genomic DNA.
DR EMBL; AL021937; CAI19588.1; -; Genomic DNA.
DR EMBL; AL021937; CAI19334.1; JOINED; Genomic DNA.
DR EMBL; Z71183; CAI19334.1; JOINED; Genomic DNA.
DR EMBL; AL021937; CAI18783.1; JOINED; Genomic DNA.
DR EMBL; AL035068; CAI18783.1; JOINED; Genomic DNA.
DR EMBL; AL035068; CAI19588.1; JOINED; Genomic DNA.
DR EMBL; Z71183; CAI19588.1; JOINED; Genomic DNA.
DR EMBL; ENSG0000100225; Homo sapiens.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00256; FBOX; 1.
DR PROSITE; PS50181; FBOX; 1.
FT NON TER
FT SEQUENCE 528 AA; 58298 MW; 467F46F7314E1F86 CRC64;
Query Match 91.9%; Score 2532; DB 2; Length 528;
Best Local Similarity 100.0%; Pred. No. 2.4e-163;
Matches 481; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 42 SNTRFTITLYNKDPLTGDEETLASVIGVSGDLICILLODDIPAPNIPSTSEHSSLQNN 101
Db 48 SNTRFTITLYNKDPLTGDEETLASVIGVSGDLICILLODDIPAPNIPSTSEHSSLQNN 107
Qy 102 EQPSLATSSNQTSMQDEQPSDSFQGAQSGVWDDSLGPGSQNFEAESIQDNAPHAEGT 161
Db 108 EQPSLATSSNQTSMQDEQPSDSFQGAQSGVWDDSLGPGSQNFEAESIQDNAPHAEGT 167
Qy 162 GFYSPPEMLCSSEVQGPVPHSLSETLYQSADCSNDALIVLHLLMLESGYIPQGTAKA 221
Db 168 GFYSPPEMLCSSEVQGPVPHSLSETLYQSADCSNDALIVLHLLMLESGYIPQGTAKA 227
Qy 222 LSPPEKWLKSGVYKLYQVHPHLCESGSSATLTCVPLGNLIVWATLKINNEIRSVKRLQLLP 281
Db 228 LSPPEKWLKSGVYKLYQVHPHLCESGSSATLTCVPLGNLIVWATLKINNEIRSVKRLQLLP 287
Qy 282 ESPICKEKLGENVANIYKDLQKLSRLFKDQVYPLLAFTQALNLPDVFGVLVPLELKL 341
Db 288 ESPICKEKLGENVANIYKDLQKLSRLFKDQVYPLLAFTQALNLPDVFGVLVPLELKL 347
Qy 342 RIFRLDVRVSLSAVCRDLFTASNDPLLWRFYLDRFRONTVTRVQDQDWKELYRKHHI 401
Db 348 RIFRLDVRVSLSAVCRDLFTASNDPLLWRFYLDRFRONTVTRVQDQDWKELYRKHHI 407
Qy 402 QRKESPKGRFVMLLPSSHTTIPFPNPLHPRFPSSRLPPGIIGGEYDQRPPLPYVGDP 461

RESULT 3
QSRBD1_PONPY
ID QSRBD1_PONPY PRELIMINARY; PRT; 443 AA.
AC QSRBD1;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFZp469H0739.
GN Name=DKFZp469H0739;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN NUCLEOTIDE SEQUENCE.
RS The German cDNA Consortium;
RC Otterwaelder B., Obermaier B., Deutschenbaur S., Schaipe A.,
RA Mewes H.W., Weill B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; CR858720; CAH90929.1; -; mRNA.
DR GO; GO:0006512; Pubiquitin cycle; IEA.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00256; FBOX; 1.
DR PROSITE; PS50181; FBOX; 1.
RW Hypothetical protein.
SQ SEQUENCE 443 AA; 49399 MW; B78AA76A054D3FED CRC64;
Query Match 80.4%; Score 2214; DB 2; Length 443;
Best Local Similarity 97.7%; Pred. No. 7.2e-142;
Matches 421; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
Qy 92 DSEHSLQNNQPSLATSSNQTSMQDEQPSDSFQGAQSGVWDDSLGPGSQNFEAESI 151
Db 13 DSEHSLQNNQPSLATSSNQTSMQDEQPSDSFQGAQSGVWDDSLGPGSQNFEAESI 72
Qy 152 QDNAPHAEGTGYSPPEMLCSSEVQGPVPHSLSETLYQSADCSNDALIVLHLLMLESG 211
Db 73 QDNAPHAEGTGYSPPEMLCSSEVQGPVPHSLSETLYQSADCSNDALIVLHLLMLESG 132
Qy 212 YIPQGTAKALSWPEKWLKSGVYKLYQVHPHLCESGSSATLTCVPLGNLIVWATLKINNEI 271
Db 133 YIPQGTAKALSWPEKWLKSGVYKLYQVHPHLCESGSSATLTCVPLGNLIVWATLKINNEI 192
Qy 272 RSVKRLQLLPESGICKEKLGENVANIYKDLQKLSRLFKDQVYPLLAFTQALNLPDVFG 331
Db 193 RSVKRLQLLPESGICKEKLGENVANIYKDLQKLSRLFKDQVYPLLAFTQALNLPDVFG 252
Qy 332 LVVLPLELKLRIIFRLDVRVSLSAVCRDLFTASNDPLLWRFYLDRFRONTVTRVQDQ 391
Db 253 LVVLPLELKLRIIFRLDVRVSLSAVCRDLFTASNDPLLWRFYLDRFRONTVTRVQDQ 312
Qy 392 WKELYRKHHIQRKESPKGRFVMLLPSSHTTIPFPNPLHPRFPSSRLPPGIIGGEYDQ 451
Db 313 WKELYRKHHIQRKESPKGRFVMLLPSSHTTIPFPNPLHPRFPSSRLPPGIIGGEYDQ 372
Qy 452 PTLPYVGDPISLIPGGETPSPQFPPLPRPDPVGLPGPNPILPGRGPNDRPFRPSR 511
Db 373 PTLPYVGDPISLIPGGETPSPQFPPLPRPDPVGLPGPNPILPGRGPNDRPFRPSR 432

```
QY 512 GRPTDGRLSFM 522
|||||
Db 433 GRPTDGRLSFM 443

RESULT 4
Q68FS3 RAT PRELIMINARY; PRT; 522 AA.
AC Q68FS3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE F-box only protein 7 (Predicted).
GN Name=Fbxo7 predicted;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RA Director MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC079382; AAH79382.1; -; mRNA.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR PROSITE; PS50181; FBOX; 1.
SQ SEQUENCE 522 AA; 57560 MW; 1A1E5C131425CD7B CRC64;

Query Match 72.0%; Score 1984; DB 2; Length 522;
Best Local Similarity 72.3%; Pred. No. 3.7e-126;
Matches 378; Conservative 57; Mismatches 86; Indels 2; Gaps 2;

QY 1 MRLRVLLKRTWPLEVPETPTGLHRLSHRLSLCTWGYSSNTRFTITLANKDPLTGDE 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MKLRLVLRKRTQPLEVPESEPTQLRAHLIQLDPLTLGFSSTRTFAITLNNKALTGDE 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 ETLASYGIVGDLICLILODDIPAPNIPSTDSSEHSSLNQNPQSLATSSNQTSDQBP 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ETLASYGIVGDLICLVLEDENPANLPSPSTDSSEHSSLNQNPQPLAATSSQANIPDEQG 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 SDSFGQAAQSGVWDDSMGLPQNFQFEASIODNAHMAEGTGFYSEPMLCSESVGGQVP 180
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 SDSHSGQVTDYDAWTDSDMEGSHGAESAIVSQDASVEASGFHPLPLEMCLCSETDGQVP 180
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 181 HSLETLYQSADCSANDALIVLHLLMLESYIPQGTAKALSMPEKWKLSGVYKLQYMH 240
||||| ||||| || ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

[illegible]

```
Db 121 QNEQSDNQKAQVEAKQSDRAGSLFFPSGLVPEDVDLEEGTGSFSEPMCLSEADGEI 180
Qy 180 PHSLETLQSDCDANDALIVLIHLLMLESGYIPQGTAKALSMPEKWKLSGVYKLYQM 239
Db 181 PHSLEVLYSABECTSDALIVLHLLMMETGVYVPGQTEAKAVSMPEKWRGNGVYKLYQT 240
Qy 240 HPLCEGSSATLTCVPLGNLIVVNTLKNINERSVKRIQLLPESFICKEKUGENVATYK 299
Db 241 HPLCEGSGAGLTCVPLGDLVAINATLKNIREIKGVKRIQLLPASVCFQGE-PEKVAGYK 299
Qy 300 DLQKLSRFLKQOLVYVPLLAFTQALNLPDVFGLVVLPLELKLRIPELLDVRSLSLSAVC 359
Db 300 DLQKLSRFLKQOLVYVSLAARQAQLNLPDVFGLVVLPLELKLRIPELLDVRSLSLSAVC 359
Qy 360 RDLFTASNDPLMLRFLYLDRFD 382
Db 360 RDLVAASNDQLLRPMYLRDRFD 382

RESULT 8
QSHYB3 HUMAN PRELIMINARY; PRT; 233 AA.
AC QSHYB3
DT 10-MAY-2005 (Tremblrel. 30, Created)
DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)
DE Hypothetical protein DKFZp686808113 (fragment).
GN Name=DKFZp686808113;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Fetal kidney;
RG The German cDNA Consortium;
RA Ottenwaelder B., Obermaier B., Deutschenbaur S., Schapp A.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX648644; CAI46263.1; -; -.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00256; FBOX; 1.
DR PROSITE; PS00181; FBOX; 1.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 233 AA; 26616 MW; 39AD4FBB26E64569 CRC64;

Query Match 45.3%; Score 1247; DB 2; Length 233;
Best Local Similarity 99.6%; Pred. No. 1.3e-76;
Matches 232; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 290 LGENVANYIKDLQKLSRFLKQOLVYVPLLAFTQALNLPDVFGLVVLPLELKLRIPELLDV 349
Db 1 LGENVANYIKDLQKLSRFLKQOLVYVPLLAFTQALNLPDVFGLVVLPLELKLRIPELLDV 60

Qy 350 RSVLSLSAVCRDLFTASNDPLMLRFLYLDRFDNTVRVQDTPDWKELYRKRHTQRKESPKG 409
Db 61 RSVLSLSAVCRDLFTASNDPLMLRFLYLDRFDNTVRVQDTPDWKELYRKRHTQRKESPKG 120

Qy 410 RVMLLPSSHTTIPYPNPLHPRPFPSSRLPGIIGGYDQRTPTLPYVGDPISLIPGPG 469
Db 121 RVMLLPSSHTTIPYPNPLHPRPFPSSRLPGIIGGYDQRTPTLPYVGDPISLIPGPG 180

Qy 470 ETPSOPPLPRPFDVPGVLPNGNPIILPGRGNDPRFPSPRGRPTDGRLSFM 522
Db 181 ETPSOPPLPRPFDVPGVLPNGNPIILPGRGNDPRFPSPRGRPTDGRLSFM 233

RESULT 9
Q6DE59_XENLA PRELIMINARY; PRT; 478 AA.
AC Q6DE59
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DE Fbox7-prov protein.
GN Name=fbox7-prov;
OS Xenopus laevis (African clawed frog);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Embryo;
RG Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Embryo;
RG Klein S., Gerhard D.S.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC077283; AAH77283.1; -; mRNA.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001226; Flavodoxin.
DR Pfam; PF00646; F-box; 1.
DR PROSITE; PS00181; FBOX; 1.
DR PROSITE; PS00201; FLAVODOXIN; UNKNOWN 1.
SQ SEQUENCE 478 AA; 53251 MW; 8C12F01E32C1873F CRC64;

Query Match 40.8%; Score 1125; DB 2; Length 478;
Best Local Similarity 47.5%; Pred. No. 6.7e-68;
Matches 251; Conservative 74; Mismatches 14; Indels 56; Gaps 14;

Qy 1 MRLRVLLKRTWPLEVPEPETGLHLRSHLSLLCTGWYGSNRTFTITLNYKDLPTGDE 60
Db 1 MRLRVVRKQTSRLEAEAEQPTGLDLRSKLSVTLPSLGSAAETHFTITLNGKDALTEQ 60

Qy 61 ETLASVGVSGDLICLILOD--DIPAPNIPSSITSEHSLQNNQOPSLSATSSNOTSMODE 118
Db 61 TTLESAGIISGDLIVVLLPDSFQIAPPAPERD-PRCPLEDPTQ-----CSTANK 111

Qy 119 QPSDSFGQAAQSGVWYNDSDMLGPSQNFESIQDNAHMAEGTGYPYS-EPMLCSSEVGE 177
Db 119 QPSDSFGQAAQSGVWYNDSDMLGPSQNFESIQDNAHMAEGTGYPYS-EPMLCSSEVGE 177
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RESULT 9

Q6DE59_XENLA

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Db 112 RP-----KGHADNEGA-----GAMPQAEASPSLDDVAM-EGQLSGPAWEVWMLCSEAVDG 159
Qy 178 QVPHSLETLYQSADCSANDALIVLIHLLMESGYIPOQTEAKALSMPEKWLKSGVYKIQ 237
Db 160 KIPHSLEVLYQTASCSASDAFIVIVHLLMLETGYLHGAETKALCMRDRWSGGAYRLH 219
Qy 238 YHPLCEGSSATLTCVPLGNLVNATUKINNEIRSVKRLQLLPSPFCCKKLGKGNVANI 297
Db 220 YTHPLCAVSATVLCPLMGKLVIIINATWKINSEKSVKRLQLLTNSYISYPETDNNVASV 279
Qy 298 YKDLQKLSRLFKDQLVLYPLLAFTTQALNLPDVGVLVPLLEKLFIFELLVRSVLSLSA 357
Db 280 YKDLQKLSGQFKDQVAYPELLAAARQVNLDPDVGVLVPLLEKLFIFELLDIRSLNLISA 339
Qy 358 VCRDLFTASNDPLLRFLYLRDRDNTVRVQDTWKELYRKRHIQRKESPKGRFV---ML 414
Db 340 TKCELLADTDPSLWRFLCIRDFRNSLPRLNGTDWKLYKEFKQKMD--RNRVFRQFL 397
Qy 415 LPSSTHTTIPFPNPLHPRFPSSRLPGIIGGEYDQRPTLPYVGDPISSLIPGPGETPSQ 474
Db 398 PPRNAHPYYPYN-VFP---PDINYPPIIGGDYDQRPPPIV-----NPTH 440
Qy 475 FPPLRPFRDPVGLPGPNPLPGRGPNDRFPFRSGRPTDGRLSFM 522
Db 441 LNP-----FKVTLPPSENDPSIPGSSG-----LRPSRGRGDIRRGFI 478

RESULT 10
Q5PQ43_XENLA
ID Q5PQ43_XENLA PRELIMINARY; PRT; 472 AA.
AC Q5PQ43;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE LOC495987 protein.
GN Name=LOC495987;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RA initiative.";
RA Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Narusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.,
RA Fahy J., Heltón E., Kettman M., Madan A., Rodríguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodríguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "generation and initial analysis of more than 15,000 full-length human
RA and mouse cdna sequences.";
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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RA Klein S., Gerhard D.S.;
RA Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC087373; AAH87373.1; -, mRNA.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR001810; P-box.
DR Pfam; PF00645; P-box; 1.
DR SMART; SM00256; FBOX; 1.
DR PROSITE; PS00181; FBOX; 1.
SQ SEQUENCE 472 AA; 52511 MW; 05EBC51A0D86F7BB CRC64;

Query Match 38 5%; Score 1059; DB 2; Length 472;
Best Local Similarity 44.2%; Pred. No. 2e-63;
Matches 234; Conservative 81; Mismatches 150; Indels 64; Gaps 13;

Qy 1 MLRLVRLKRTWPLEVPEPTLGLHSLRLSLLLCTGWYSSNTRFTITLNYKDLPTGDE 60
Db 1 MCLRVRVRKQTRLDLEAEQPTLGDVRSKLSVTLPALGYSAETDFTITLNGKDLTGDO 60
Qy 61 ETLASYGIVSGDLICLILQDDIPAPNIPSTSDSEHSLQNNQPSLATSSNQTSMQDEQP 120
Db 61 TALEAGIISGDLIILLPDS-PIPPPPAPE-----RRDPRCPLEDPTQHCSTALKRP 113
Qy 121 SDSFGQAAQSGYV-NDDSMLGPSQNEAESIQDNAHWAEGTGFPYS---EPMLCSSEVE 176
Db 114 KGVNNDGAKAQRVPQTEAAEETSPSMEDVTMEDT-----PSPAEVWMLCSEAVD 164
Qy 177 GOVPHSLETLYQSADCSANDALIVLIHLLMESGYIPOQTEAKALSMPEKWLKSGVYK 236
Db 165 GKIPHSLEVLYQTASCSASDAFIVIVHLLMLETGYLQGAESKALCMRDRWSGGAYRL 224
Qy 237 QYHPLCEGSSATLTCVPLGNLVNATUKINNEIRSVKRLQLLPSPFCCKKLGKGNVAN 296
Db 225 HYTHPLCAQVSATLACLPMGKLVIN-----DNDPAS 256
Qy 297 IYKDLQKLSRLFKDQLVLYPLLAFTTQALNLPDVGVLVPLLEKLFIFELLVRSVLSLS 356
Db 257 YKDLQKLSGQFKDQVAYPELLAAARQVNLDPDVGVLVPLLEKLFIFELLDIRSLNL 316
Qy 357 AVCRDLTASNDPLLRFLYLRDRDNTVRVQDTWKELYRKRHIQRKESPKGRFV---M 413
Db 317 ATCKELLAAAGDSLSLWRFLCIRDFRNSLPRLNGTDWKLYKEFKQKMD--RNRVFR 374
Qy 414 LPSSTHTTIPFPNPLHPRFPSSRLPGIIGGEYDQRPTLPYVGDPISSLIPGPGETPS 473
Db 375 LPPRNAHPYYPYN-IFP---PDFSVYPPIIGGEYDQRPPPIV-NPTAFPIGVGPSSS 429
Qy 474 QFPPLRPFRDPVGLPGPNPLPGRGPNDRFPFRSGRPTDGRLSFM 522
Db 430 RFSPLSNPFKVTLPPSEEDPSIP---GPRS---LRPSRGRGDIRRGFI 472

RESULT 11
Q4V8X6_BRARE
ID Q4V8X6_BRARE PRELIMINARY; PRT; 486 AA.
AC Q4V8X6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE LOC558097;
DE Hypothetical protein LOC558097.
GN Name=LOC558097;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettunen M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (2)
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RG NIH MGC Project;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC097156; AAH97156.1; -, mRNA.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00256; FBOX; 1.
DR PROSITE; PS0181; FBOX; 1.
KW Hypothetical protein.
SQ SEQUENCE 486 AA; 53896 MW; 367C5FAD32BB0CC CRC64;

Query Match 31.8%; Score 877; DB 2; Length 486;
Best Local Similarity 39.1%; Pred. No. 4.7e-51;
Matches 212; Conservative 89; Mismatches 165; Indels 76; Gaps 15;
QY 1 MRLVRLKRTWPLEVETPTLGHRLSHRLSLCTGWYSSNTFTITLNYKDLPTGDE 60
DB 1 MRLVRLSHRQICRLQLQGEPSLAELARVRESLLTRFLRSLDLDRLSLNGKEDLLDTG 60
QY 61 ETLASGVISGDLICLILODDIPAPNIPSPSTDSHSSLONNQPSLATSSNQTSMQ---- 116
DB 61 QSLSCGVSGDLISVIL-----PA-----SSLEETQTSAAAHQTHTDQAGGS 105
QY 117 DEQSDSPGQAAQSGVWNDSDMLGPSQNFPAESIQDNA-----HMAEGTFYFSEPMLCES 171
DB 106 HVSSSSSVMEQHVQSERV-DQDLLEVRVQDQCEVDLQDQDQCEVCVCAAPPLLC 164
QY 172 SESVEGVPHSLLETLYQSADCSANDALIVLHLLMLESYIPQGTAKALSMPEKWKLS 231
DB 165 CEADGLPLALERLSDSTCRSPSDCLMLALHLLLETGFIPOGGAVSSGEMPIGWQAA 224
QY 232 -GVYKLYQVHPICGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKEL 290
DB 225 GGVFLQVHPHLLNSLVSVAVPMGQTLVINAVLKMETSLENSRKLLKLPDEYVTAET 284
QY 291 GENVANIYKDLQKLSRLFKDQVYPLLAFTQALNLPDVFGVLVPLLEKLIRIFRLDVR 350
DB 285 GGSQGVYRDLRLSRLVRDQVYPLMATARQALGLPLFLGVLPELLLRLLRLDVR 344
QY 351 SVLSAVCRDLFTASNDPLLRFLYLRDRFNTV---RVQDTHKELYRKHIORKESP 407
DB 345 SVLSAVACRHLNTATHDASLRHLLHLLDRFRVSPFAGHQHRTDWRRELYKQYRQKGA 404
QY 408 -KGRFVMLPSSTHTIPFPNPLHPR-PFPSS-----RLPPGIIGGYDQRTPLVVGDP 460
DB 405 RGRG-----HW--FYPFISPLIPFPSSAPLPPLYPPIIGGYDQMPV----- 446
QY 461 ISSLIPGPGTSPQFPPLRPDPVGLPGPNPILPGRGPNDRFPFRSGRPTDGLRLS 520
DB 447 ---ILP-----RPRFHPGIP-----LPGMSAPVGRSLRSPAGSGAADVRA 484

QY 521 FM 522
DB 485 FI 486
RESULT 12
Q5SPK1_BRARE PRELIMINARY; PRT; 483 AA.
AC Q5SPK1;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Novel protein similar to mouse and human F-box protein 7 (FBOX07).
GN ORFNames=CH211-286M4.2-001;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RA Phillimore B.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AL845512; CAI12002.1; -, Genomic DNA.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00256; FBOX; 1.
DR PROSITE; PS0181; FBOX; 1.
SQ SEQUENCE 483 AA; 53554 MW; 350DB1744D2E05D1 CRC64;

Query Match 31.7%; Score 873.5; DB 2; Length 483;
Best Local Similarity 39.4%; Pred. No. 8.1e-53;
Matches 210; Conservative 90; Mismatches 172; Indels 61; Gaps 14;
QY 1 MRLVRLKRTWPLEVETPTLGHRLSHRLSLCTGWYSSNTFTITLNYKDLPTGDE 60
DB 1 MRLVRLSHRQICRLQLQGEPSLAELARVRESLLTRFLRSLDLDRLSLNGKEDLLDTG 60
QY 61 ETLASGVISGDLICLILODDIPAPNIPSPSTDSHSSLONNQPSLATSSNQTSMQ---- 116
DB 61 QSLSCGVSGDLISVIL-----PA-----SSLEETQTSAAAHQTHTDQAGGS 105
QY 117 DEQSDSPGQAAQSGVWNDSDMLGPSQNFPAESIQDNA-----HMAEGTFYFSEPMLCES 174
DB 106 HVSSSSSVMEQHVQSERV-DQDLLEVRVQDQCEVDLQDQDQCEVCVCAAPPLLC 164
QY 175 VEGQVPHSLLETLYQSADCSANDALIVLHLLMLESYIPQGTAKALSMPEKWKLS-GV 233
DB 165 EDGLPLALERLSDSTCRSPSDCLMLALHLLLETGFIPOGGAVSSGEMPIGWQAGGV 224
QY 234 YKLYQVHPHLLNSLVSVAVPMGQTLVINAVLKMETSLENSRKLLKLPDEYVTAET 293
DB 225 FRLOVYHPHLLNSLVSVAVPMGQTLVINAVLKMETSLENSRKLLKLPDEYVTAET 284
QY 294 VANITYKDLQKLSRLFKDQVYPLLAFTQALNLPDVFGVLVPLLEKLIRIFRLDVR 353
DB 285 GGVFLQVHPHLLNSLVSVAVPMGQTLVINAVLKMETSLENSRKLLKLPDEYVTAET 344
QY 354 SVLSAVCRDLFTASNDPLLRFLYLRDRFNTV---RVQDTHKELYRKHIORKESP-KG 409
DB 345 SVLSAVACRHLNTATHDASLRHLLHLLDRFRVSPFAGHQHRTDWRRELYKQYRQKGA 404
QY 410 RFWMLPSSTHTIPFPNPLHPRFPSSRLPPIIGGYDQRTPLPYVGDIPISLIPG 469
DB 405 RHWFPPIISLIPF-PSP--PAPLP--LYPPGIIGGYDQMPV-----LIP--- 446
QY 470 ETPSQFPLRPDPVGLPGPNPILPGRGPNDRFPFRSGRPTDGLRSLF 522
DB 447 -----RPRFHPGIP-----LPGMSAPVGRSLRSPAGSGAADVRAFI 483

RESULT 13

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Q478W7_TETNG
ID Q478W7_TETNG PRELIMINARY; PRT; 471 AA.
AC Q478W7;
DT 13-SEP-2005 (TEMBLrel. 31, Created)
DT 13-SEP-2005 (TEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF7713, whole genome shotgun sequence.
GN ORFNames=GSTENG0005041001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraontoidea; Tetraodontidae; Tetraodon.
ON NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Castolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: CAAE01007713; CAF90665.1; -: Genomic DNA.
SQ SEQUENCE 471 AA; 50502 MW; 498364ASCEI31930 CRC64;

Query Match 30.9%; Score 851.5; DB 2; Length 471;
Best Local Similarity 38.9%; Pred. No. 2.4e-49;
Matches 209; Conservative 76; Mismatches 171; Indels 81; Gaps 17;

QY 1 MRLRVLLKKTWPLEVPEPTETPTGLHLSHLRLSLCTWGSYNNTRFTITLNYKDLPTGDE 60
DB 1 MRLRVVQGGKTSLELQGEERFLAELVLLRVVLPVSVGLSAETQFGSLNGSEVLEDTG 60

QY 61 ETLASYGIVSGDILCLIQDIPAPNTPSSTDSEHSLQNEOPLSATSSNOTSMQDEQP 120
DB 61 QALASCGVSGDLVRVVLDD--PAAQAPRAASHQRG-----PAQEVATETPASHTEQP 111

QY 121 SDSFQGAAGSGVNMDDSLGPSQNFPAESIQDHAHAETGTPYS--EPMLCSESVEGQV 179
DB 112 SDHGEAGAP-----AGPAPGWE-----PGWPEMLCSEADAGQA 144

QY 180 PHSLETYQSGADCSNDALIVLHLLMLSEGYIPQGTAKALSMPEKWL--SGVYKLQY 238
DB 145 PLSLELLFHSAGVGAADAVAAAHLLMVETGTPQGCCELKSDMPAGMRCGGGVYRLQY 204

QY 239 MHPLECGSSATLCTVPLGNLIVNATIKINNEIRSVKRLQLLPESFICKELGENVANIY 298
DB 205 SHRLCGSVVMVAVSUGSLAIIISGLLEVNSQSDSVCKLSLEPSSVYTEAMPDGSAAAF 264

QY 299 KDLQKLSRLFKDQLVYPLLAFTRAQLMLPDVFGVLVPLLELKLRIFFLLDVRVLSLSAV 358
DB 265 KDLKLSRVFKDQVAYPLITASHRHVALPEVFGLTALPPELLLRVLELLDVRVSLRAAV 324

QY 359 CRDLFTASNDPLVFLYLRDFR--DNTVRVODDTWELKRYKRRIHQKESPKGRFVMLLPS 417
DB 325 CRHLGAITSRLALRWHLRYCDRFGSHAGSRDQTQWKELYQQAYRRRLQPP-----PQ 376
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QY 418 STHTIPFP---NP---LHPRPFPSSRLP--PGIIGGEYDQRTLPYVGDPISSLIPGP 469
DB 377 RLH-----YPCLDPRALHPPF-----FPPVPGIIGGEYDQSPFP-----G 416

QY 470 ETPSQPPLPRPDPVGPLPG-----NPIPLPGGPNDRPFPSPRSRPTDGRLSFM 522
DB 417 PLPQGVLP-RPRYDPMSPFPDLDRRPPTISEGAWGCGGARRPG-CGGADVRRGFI 471

RESULT 14
Q9ZUB8_ARATH
ID Q9ZUB8_ARATH PRELIMINARY; PRT; 475 AA.
AC Q9ZUB8;
DT 01-MAY-1999 (TEMBLrel. 10, Created)
DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
DT 01-FEB-2005 (TEMBLrel. 29, Last annotation update)
DE F508.33 protein (At1g23780/F508_31).
GN Name=F508.33;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OC NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Liu S., Lenz C.,
RA Li J., Kremenskaia I., Luros J., Altafi H., Gonzalez A., Araujo R.,
RA Buehler E., Conn L., Conway A.B., Dunn P., Hansen N., Huizar L.,
RA Kim C., Palm C.J., Rowley D., Shinn P., Walker M., Davis R.W.,
RA Ecker J.R., Federspiel N.A., Theologis A.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Theologis;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P.,
RA Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,
RA Huan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,
RA Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
RA Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC005990; AAC98033.1; -: Genomic DNA.
DR EMBL: AY049291; AAK83633.1; -: mRNA.
DR EMBL: AY149929; AAN31083.1; -: mRNA.
DR PIR: A86372; A86372.
GO: GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR002052; N6_Mtase.
DR Pfam: PF00646; F-box; 1.
DR SMART: SM00256; FBOX; 1.
DR PROSITE: PS0181; FBOX; 1.
DR PROSITE: PS00092; N6_MTASE; UNKNOWN 1.
SQ SEQUENCE 475 AA; 52947 MW; D068CCFI5448BFC3 CRC64;

Query Match 8.7%; Score 240.5; DB 2; Length 475;
Best Local Similarity 24.5%; Pred. No. 7.4e-08;
Matches 116; Conservative 89; Mismatches 177; Indels 91; Gaps 20;
```

QY 1 MRLRVLLKRTWPLEVPETEPTLGHLSRLSLICTWGYSSNTRFTITLANKDPL--TG 58
Db 3 LRLRHETRETKLELAAD--TLHDLRRINPTV-----PSSVHLISLNRKDELITPS 53
QY 59 DEETLASYGIVSGDLICILQDDIPAPNIPSTDSHSSLOQNEQPSLATSSNQTSMODE 118
Db 54 PEDTLRSGLISGLIYFSLE-----AGESSNWKLRDSETVASQSESNQTSVHD- 102
QY 119 QPSDSFOQAAGSGVWDDSMGLPSONFEASIQONAHMAEG--TGFPSPBM----- 169
Db 103 --SIGF-----AEVDVVPQAKSNPN-----TSVED-----PEGDISGMEGPEPMDVEQLDM 147
QY 170 --LCSSEVEGQVPHSLET--LYQSDACSDANDALIVLIHLMLESGYI--PQGT----- 218
Db 148 ELAAGSKRLSEPPFLKNILKESGDTSELT--TLALSIVHAWLSEGFVLLNHGSKFNFS 206
QY 219 AKALSMPEKWKLSGVYKLYQMHPKCEGSSATITCPLGNLIVVNA TL-----KINNEI-- 271
Db 207 KELLTVSLRYTLPELIKSDNTI---ESVSVKFQNLGPPVVVYVYCTVGSSGRVHMNLDK 263
QY 272 -RSVKRLQLLPESFICKELGENVANIYKDLQKLSRLFKDQLVYPLLAFTQALNLPDVF 330
Db 264 RRFVPVIDLMDTSDSDE---EGSSSIYREVFMFWMVKDRLVIPLLIIGICDKAGLEPPP 320
QY 331 GLVVLPLELKLRIFFELLDVRSVLSLAVCRDLFTASNDPDLWRFLYLRDRDNTVRV--Q 388
Db 321 CLMLRPLELKLLELLPGVSGNMACVCTEMRYLASNDLWKQKCLEEVNFFVTEAGD 380
QY 389 DTDWK-----ELYKRHHIORKESPGRFVWMLPSPSTHTTIPF 424
Db 381 SVNWKARFATWRQKLAASDTPFRQNLGRNISTGRSGIRPRIIGDPPF 433

RESULT 15
Q8GZV6 ORYZA
ID Q8GZV6 ORYZA PRELIMINARY; PRT; 776 AA.
AC Q8GZV6
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Hypothetical protein OJ1017C11.10.
GN Name=OJ1017C11.10;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Currie J.,
RA Collura K.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AC135157; AA000689.1; -; Genomic_DNA.
DR Gramene; Q8GZV6; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0030528; P:transcription regulator activity; IEA.
DR GO; GO:0006464; P:protein modification; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR000209; Pept_S8_S53.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00010; HLH; 1.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00213; UBQ; 1.
DR PROSITE; PS50181; FBOX; 1.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS00136; SUBTILASE ASP; UNKNOWN_1.
DR PROSITE; PS50053; UBIQUITIN_2; 1.

KW Hypothetical protein.
SQ SEQUENCE 776 AA; 83302 MW; F05B3429D2B924BD CRC64;
Query Match 7.4%; Score 205; DB 2; Length 776;
Best Local Similarity 22.0%; Pred. No. 3.8e-05;
Matches 115; Conservative 90; Mismatches 197; Indels 120; Gaps 25;
QY 1 MRLRVLLKRTWPLEVPETEPTLGHLSRLSLICTWGYSSNTRFTITLANKDPL 51
Db 1 MKLRLSMQDQGGAGGAETHRVOLPDT--ATLSVVKAFPLATKLSAAQVPVPAES--VRLTLN 58
QY 52 YKDP-LTGD--EETLASYGIVSGDLICILQDDIPAPNIPSTDSHSSLOQNEQPSLATSSNQTSMODE 106
Db 59 RSEELLTPDPSATLPA LGLASGLIYFTL--SPLSPSPPPPPQPPQQAQPLRPNPDVFSI 117
QY 107 ATSSNQTSMDQSDSFQQAAGSG---VWDDSMGLPSONFEASIQONAHMAEGTG 162
Db 118 AGAADPTKSPVESGSSSSMPQALCTNPGLPVASDPHPPP-----DVVMAEAF 166
QY 163 FYPSEPMLCSESVGQVPHSLETLYQSD---CSDANDALIVLIHLMLESGYI PQGT 218
Db 167 VIKSK---SSLVVGDTKREMN--GGADGTVIC-----RLVVALHAALLDAGFLYANPV 216
QY 219 AKALSMPEKWKLSGVY---KLYQMHP-----LCBSSATLTCVPLGNLIVVNA TLKI 267
Db 217 GSCIQLPQNW--ASGFVPVSMKYTLPELVEALPVVEGMAVAVLSLGNFMVVG--HV 273
QY 268 NNEIRSVKRL-----QLLPSEFICKELGENVANIYKDLQKLSRLFKDQLVYPLLAFTQ 322
Db 274 PGATSGVRRLCLELPELAPLLYLDSDVSTAEE---REIHELWRVLKDEMCLPLMISLCQ 330
QY 323 ALNLPDVFGLVVLPLELKLRIFFELLDVRSVLSLAVCRDLFTASNDPDLWRFLYLRDRD 382
Db 331 LNNLSLPPCLMALPGDWAKVLEFPVGVDLARVQCTCKELRDLAADDNLWKKCEMEF-- 388
QY 383 NTVRVQDT---DWKELY---RK-----RHIQRKESPKGRFVWMLL----- 415
Db 389 NT---QDTGCGMCKCIYSQDKDVLADKYTCGNYMCKPVTQFGRWLIILVYHSLLCQY 445
QY 416 -----PSSHTHTTIPFPNPLHPRFPSS 437
Db 446 ITIGLSLLWVHLVDLVQDAPAAAGIHFDCCIIPLPINPYQLPPS 487

Search completed: February 14, 2006, 21:01:47
Job time : 238 secs

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OM protein - protein search, using sw model

Run on: February 14, 2006, 20:54:24 ; Search time 189 Seconds
(without alignments)
1213.522 Million cell updates/sec

Title: US-09-927-458-2
Perfect score: 2754
Sequence: 1 MRLVRLKRTWPLEVETE.....DRFFRPSRGRTDGRLSFM 522

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003s.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2748	99.8	522	6	ADA57283 Human sec
2	2748	99.8	522	6	ADA41163 Human sec
3	2748	99.8	522	6	ABR47958 Human sec
4	2748	99.8	522	7	ADC74366 Human sec
5	2744	99.6	522	4	AB35161 Human Skp
6	2744	99.6	522	8	ABM82342 Tumour-as
7	2744	99.6	522	8	ADU46626 Human Fbx
8	2744	99.6	522	9	ADZ70638 Human pro
9	2510	91.1	591	2	AAW68521 Human RIP
10	2489	90.4	482	3	AA83047 F-box pro
11	2489	90.4	482	3	AAO22452 Human F-b
12	2489	90.4	482	9	ADY62371 Human F-b
13	2448.5	88.9	607	4	AAU32109 Novel hum
14	2404	87.3	462	5	ABB90109 Human pol
15	2404	87.3	462	6	ADA57586 Human sec
16	2404	87.3	462	6	ADA41482 Human sec
17	2404	87.3	462	6	ABR48139 Human sec
18	2404	87.3	462	7	ADC74596 Human sec
19	2270	82.4	443	4	AB35160 Human Skp
20	2086.5	75.8	549	4	ABG18510 Novel hum
21	1527	55.4	317	5	ABB90108 Human pol
22	1238	45.0	231	7	ADJ68946 Human hea
23	1086	39.4	221	6	ADA54155 Human pro
24	714	25.9	174	6	ADA57587 Human sec

25	714	25.9	174	6	ADA41483	Ada41483 Human sec
26	714	25.9	174	6	ABR48140	Abz48140 Human sec
27	714	25.9	174	7	ADC74597	Adc74597 Human sec
28	714	25.9	175	2	AA411397	AAy411397 Human sec
29	502	18.2	94	4	AAU32107	AAu32107 Novel hum
30	396	14.4	76	8	ABO54274	ABO54274 Human gen
31	299	10.9	113	3	AA87356	AAy87356 Human sig
32	265.5	9.6	225	4	ABG06838	ABg06838 Novel hum
33	264.5	9.6	53	4	ABG18509	ABg18509 Novel hum
34	264.5	9.6	53	4	AAU32108	AAu32108 Novel hum
35	249	9.0	47	8	ABO59862	ABO59862 Human gen
36	240.5	8.7	475	3	AA829404	AAg29404 Arabidops
37	215.5	7.8	500	8	ADT59833	Adt59833 Plant poi
38	211	7.7	485	8	ADX97246	Adx97246 Plant ful
39	207	7.5	485	8	ADX96467	Adx96467 Plant ful
40	201	7.3	485	8	ADY05169	Ady05169 Plant ful
41	194	7.0	39	3	AA83054	AAy83054 F-box mot
42	194	7.0	39	5	AAO22459	AAo22459 Human F-b
43	194	7.0	39	9	ADY62378	Ady62378 F-box mot
44	189	6.9	38	2	AAU02272	AAy02272 A F-box p
45	189	6.9	38	4	AAE08044	AAe08044 Human F-b

ALIGNMENTS

RESULT 1
ADA57283
ID ADA57283 standard; protein; 522 AA.
XX
AC ADA57283;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human secreted protein #566.
XX
KW immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
KW cytosolic; cerebroprotective; neuroprotective; nootropic;
KW cardiovascular; antiarteriosclerotic; gene therapy;
KW human secreted protein; immune disorder; inflammation;
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KW triple helix formation; antisense gene therapy; forensic biology.
XX
OS Homo sapiens.
XX
FN WO2002102994-A2.
XX
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US0008278.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
XX WPI; 2003-167512/16.
XX
XX N-PSDB; ADA56387.
XX
XX New human secreted polypeptides and polynucleotides, useful for
XX diagnosing, treating or preventing e.g. immune disorders, inflammatory
XX conditions, respiratory disorders, cancers, CNS disorders, or
XX neurodegenerative disorders.
PS Claim 13; SEQ ID NO 1473; 1754pp; English.
XX
CC The invention relates to 592 new human secreted polypeptides useful for

diagnosing, treating or preventing e.g. immune disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, or neurodegenerative disorders, or polypeptides comprising an amino acid sequence at least 95% identical to the new sequences. The polypeptides, antibodies or antibody fragments that bind to the polypeptides, nucleic acids encoding the polypeptides, agonists or antagonists that binds to the polypeptide, are useful in preparing diagnostic or pharmaceutical compositions for diagnosing, treating or preventing an e.g. immune disorders, inflammatory conditions (e.g. inflammatory bowel disease, nephritis or Crohn's disease), respiratory disorders (e.g. asthma and allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative disorders (e.g. Parkinson's disease or Alzheimer's disease), and cardiovascular disorders (e.g. atherosclerosis or myocarditis). The polynucleotides are useful for chromosome identification, chromosome mapping, for controlling gene expression through triple helix formation or antisense DNA or RNA, in gene therapy, for identifying individuals from minute biological samples, in forensic biology, and as hybridization probes. The polypeptides are useful for as molecular weight markers on sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) gels, to raise antibodies, for testing biological activities, and for treating or preventing neural disorders, immune system disorders, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, proliferative and/or cancerous diseases. This sequence corresponds to one of the polypeptide of the invention. Note: The sequence data for this patent did form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 522 AA;

Query Match 99.8%; Score 2748; DB 6; Length 522;

Best Local Similarity 99.8%; Pred. No. 6.5e-239; Mismatches 1; Indels 0; Gaps 0; Matches 521; Conservative 0;

Qy 1 MRLVRLKRTWPLEVPEPTETLGHRLSHLRLSLCTWGYSSNTRFTITLKYDPLTGDE 60
Db 1 MRLVRLKRTWPLEVPEPTETLGHRLSHLRLSLCTWGYSSNTRFTITLKYDPLTGDE 60
Qy 61 ETLASYGIVSGDLICLILODDIPAPNIPSSSTDSEHSLQNNQPSLATSSNOTSNQDQRP 120
Db 61 ETLASYGIVSGDLICLILODDIPAPNIPSSSTDSEHSLQNNQPSLATSSNOTSNQDQRP 120
Qy 121 SDSFGQQAQSGVWDDSMGLPSONFEASTODNAHMAEGTGYPSPEMLCSSEVGGVP 180
Db 121 SDSFGQQAQSGVWDDSMGLPSONFEASTODNAHMAEGTGYPSPEMLCSSEVGGVP 180
Qy 181 HSLETLYQSADCSANDALIIVLHLLMESGYIPOGTEAKALSMEKWKLSGVYKLYQYMH 240
Db 181 HSLETLYQSADCSANDALIIVLHLLMESGYIPOGTEAKALSMEKWKLSGVYKLYQYMH 240
Qy 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFTCKEKLGENVANIYKD 300
Db 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFTCKEKLGENVANIYKD 300
Qy 301 LOKLSRLPKDQVLPFLAFTQALNLPVFGVLVPLFLKLRIFLLDVRSVLSAVCR 360
Db 301 LOKLSRLPKDQVLPFLAFTQALNLPVFGVLVPLFLKLRIFLLDVRSVLSAVCR 360
Qy 361 DLFTASNDPLLRFLYLRDFRNTVRVQDQTKELYRKRHQRKESPKGRFVMLLPSSSTH 420
Db 361 DLFTASNDPLLRFLYLRDFRNTVRVQDQTKELYRKRHQRKESPKGRFVMLLPSSSTH 420
Qy 421 TTPYPNPLHRRPPSSRLPGIIGGEYDQRTPLPYVGDPISLLIPGGETPSQPPLRP 480
Db 421 TTPYPNPLHRRPPSSRLPGIIGGEYDQRTPLPYVGDPISLLIPGGETPSQPPLRP 480
Qy 481 RFDVPGLPGNPILPGGGPNDRFPFRSGRPTDGRLSFM 522
Db 481 RFDVPGLPGNPILPGGGPNDRFPFRSGRPTDGRLSFM 522

RESULT 2

ADA41163
ID ADA41163 standard; protein; 522 AA.
XX
AC ADA41163;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human secreted protein.
XX
KW Human; secreted protein; cancer; hyperproliferative disorder;
KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
KW anaemia; allergic reaction; asthma; cardiovascular disorder;
KW wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;
KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
KW vulnery; cardiant; gene therapy.
XX
OS Homo sapiens.
XX
WO2002102993-A2.
XX
PD 27-DEC-2002.
XX
XX 19-MAR-2002; 2002WO-US008123.
XX
XX 21-MAR-2001; 2001US-0277340P.
XX
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-175238/17.
XX
PT New human secreted proteins and nucleic acid molecules, useful for preparing a diagnostic or pharmaceutical composition for diagnosing, preventing or treating cancer or other hyperproliferative disorder, asthma, allergies or AIDS.
XX
PS Claim 1; SEQ ID NO 1545; 3205pp; English.
XX
CC The invention relates to novel genes ADA39629-ADA40565 and proteins ADA40566-ADA41501 for human secreted proteins, useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The polypeptides, nucleic acid molecules, antibodies or their fragments, and agonists or antagonists that bind to the polypeptide are useful for preparing a diagnostic or pharmaceutical composition for diagnosing or treating cancer or other hyperproliferative disorder. The polypeptides and nucleic acid molecules are also useful for detecting, preventing, diagnosing, prognosticating, treating or ameliorating cancer or other hyperproliferative disorders including neoplasms, autoimmune disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic anaemia), haematopoietic or haematological disorders (e.g. anaemia, thrombocytopenia), allergic reactions including asthma or eczema, inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory bowel disease or Crohn's disease), neurodegenerative disorders (e.g. Alzheimer's disease or Parkinson's disease), cardiovascular disorders (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial, fungal or viral infections including HIV/AIDS), or wound healing and disorders of epithelial cell proliferation. The nucleic acids are also useful for chromosome identification, radiation hybrid mapping or long-range restriction mapping, as molecular weight markers, or as hybridization or diagnostic probes. The polypeptides and antibodies are useful for providing immunological probes for differential identification of the tissues immunohistochemistry assays. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 522 AA;

Query Match 99.8%; Score 2748; DB 6; Length 522;

Best Local Similarity 99.8%; Pred. No. 6.5e-239;		
Matches 521; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	1	MRLRVLLKRTWPLEVPEPETETGLHRLSHRLSLICTWGYSSNTRFTITLNYKDPPLTGDE 60
Db	1	MRLRVLLKRTWPLEVPEPETETGLHRLSHRLSQSLICTWGYSSNTRFTITLNYKDPPLTGDE 60
QY	61	ETLASYGIVSGDLICLIILQDDIPAPNIPSSDSEHSSLQNNQEPSLATSSNQTSMQDEQP 120
Db	61	ETLASYGIVSGDLICLIILQDDIPAPNIPSSDSEHSSLQNNQEPSLATSSNQTSMQDEQP 120
QY	121	SDSFQGAQAQGVNDDSMLGPSQNFEAESTQDNAHMAEGTGFYPSBPMLCSESVGEQVP 180
Db	121	SDSFQGAQAQGVNDDSMLGPSQNFEAESTQDNAHMAEGTGFYPSBPMLCSESVGEQVP 180
QY	181	HSLETLYQADCSANDALIVLIHLLMLESYIIPQTEAKALSMPKWKLSGVYKLOYMH 240
Db	181	HSLETLYQADCSANDALIVLIHLLMLESYIIPQTEAKALSMPKWKLSGVYKLOYMH 240
QY	241	PLCGSSATLTCVPLGNLIIVNATLKINNEIRSVKRLQLLPESFICKEKLGENVANIYKD 300
Db	241	PLCGSSATLTCVPLGNLIIVNATLKINNEIRSVKRLQLLPESFICKEKLGENVANIYKD 300
QY	301	LQKLSRLPKDQIVVPLLAFTQALNLPDVFGLVVLPELKURIIRLLDVRSLVLSAVCR 360
Db	301	LQKLSRLPKDQIVVPLLAFTQALNLPDVFGLVVLPELKURIIRLLDVRSLVLSAVCR 360
QY	361	DLFTASNDPLLRWFYLYLRDFRDNTVRVQDTPDKELYRKRHITORKESPKGRFVMLLPSSSTH 420
Db	361	DLFTASNDPLLRWFYLYLRDFRDNTVRVQDTPDKELYRKRHITORKESPKGRFVMLLPSSSTH 420
QY	421	TIPFVNPPLHPRPPFPSSRLPGIIGGEVDQRPTLPYVGDPITSSILIPGGETPSQFPPLRP 480
Db	421	TIPFVNPPLHPRPPFPSSRLPGIIGGEVDQRPTLPYVGDPITSSILIPGGETPSQFPPLRP 480
QY	481	RFDPVGPLPGNPILPGRGGNDPRPPRPSRGRPTDGRLSFM 522
Db	481	RFDPVGPLPGNPILPGRGGNDPRPPRPSRGRPTDGRLSFM 522
RESULT 3		
ABR47958		
ID	ABR47958 standard; protein; 522 AA.	
XX		
AC	ABR47958;	
XX		
DT	12-JUN-2003 (first entry)	
XX		
DE	Human secreted protein, SEQ ID 849.	
XX		
KW	Cardiant; antiarrhythmic; antiarteriosclerotic; vasotrophic; cytostatic;	
KW	vulnary; antiinflammatory; nootropic; neuroprotective;	
KW	antiparkinsonian; gene therapy; human; cardiovascular disorder.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200295010-A2.	
XX		
PD	28-NOV-2002.	
XX		
PF	19-MAR-2002; 2002WO-US009785.	
XX		
PR	21-MAR-2001; 2001US-0277340P.	
PR	19-JUN-2001; 2001US-0306171P.	
PR	13-NOV-2001; 2001US-0331287P.	
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Ruben SM;	
XX		
DR	WPI; 2003-129429/12.	
XX		
PT	Novel human secreted proteins, useful for detecting preventing	

RESULT 4

diagnosing, prognosticating, treating and/or ameliorating cardiovascular disorders such as arrhythmia.

Claim 13; SEQ ID NO 849; 1881pp; English.

The present invention relates to novel human secreted proteins (ABRA7633-CC ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins and their coding sequences are useful for the preparation of a diagnostic or pharmaceutical composition for diagnosing or treating a cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary arteriosclerosis and myocardial ischaemia), neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, pulmonary disorders, renal disorders, proliferative disorders and/or cancerous diseases and conditions, for wound healing and epithelial cell proliferation, to treat inflammation or infection, for treating thrombosis and arteriosclerosis, for treating or preventing neural damage which occurs in neuronal disorders or neurodegenerative conditions such as Alzheimer's disease and Parkinson's disease, to enhance bone and periodontal regeneration and aid in tissue transplants or bone grafts, to prevent skin aging or hair loss, to stimulate growth and differentiation of haematopoietic cells and bone marrow cells when used in combination with other cytokines, and bone organs before transplantation or for supporting cell culture of primary tissues, to increase or decrease differentiation or proliferation of embryonic stem cells, or to modulate mammalian characteristics or metabolism. Note: The sequence data for this patent was published in electronic format and is available from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

Sequence 522 AA:

Query Match	99.8%	Score	2748	DB	6	Length	522
Best Local Similarity	99.8%	Pred.	No.	6.5e-239			
Matches	521	Conservative	0	Mismatches	1	Indels	0
Gaps	0						
Qy	1	MRLRVLLKRTWPLEVETETPTGLHLSHLRLSLCTWTGYSNTRFTTILNYPKDLPTGDE	60				
Db	1	MRLRVLLKRTWPLEVETETPTGLHLSHLRQSLCTWTGYSNTRFTTILNYPKDLPTGDE	60				
Qy	61	ETLASYGIVSGDLICLILODDIPAPNIPTSDTSEHSSIQQNEQPSLATSSNQTSMQDEOP	120				
Db	61	ETLASYGIVSGDLICLILODDIPAPNIPTSDTSEHSSIQQNEQPSLATSSNQTSMQDEOP	120				
Qy	121	SDSPQQAAGSVWNDDSMIGPSQNFRAESTQDNAHMAEGTGFYPSEPMLCSESVGEQVP	180				
Db	121	SDSPQQAAGSVWNDDSMIGPSQNFRAESTQDNAHMAEGTGFYPSEPMLCSESVGEQVP	180				
Qy	181	HSLETLQSQADCSANDALIVLIHLLMLESYIIPQGETAKALSMPKWKLSGVYKLYQNM	240				
Db	181	HSLETLQSQADCSANDALIVLIHLLMLESYIIPQGETAKALSMPKWKLSGVYKLYQNM	240				
Qy	241	PLCEGSSATLTCVPLGNLIYVNATLKINNEIRSVKRLQLLPESPTICEKLGENVANIYKD	300				
Db	241	PLCEGSSATLTCVPLGNLIYVNATLKINNEIRSVKRLQLLPESPTICEKLGENVANIYKD	300				
Qy	301	LQKLSRFLKQOLVYPLLAFTRAQLNLPDVFGLVVLPLELKURIIRLLDVRSVLSLSAVCR	360				
Db	301	LQKLSRFLKQOLVYPLLAFTRAQLNLPDVFGLVVLPLELKURIIRLLDVRSVLSLSAVCR	360				
Qy	361	DLFTASNDPILWRFLYLDRDRDNTVRQDITDWKELYRKRHITORKESPKGRFVMLLPSSSTH	420				
Db	361	DLFTASNDPILWRFLYLDRDRDNTVRQDITDWKELYRKRHITORKESPKGRFVMLLPSSSTH	420				
Qy	421	TIFPYNPMLHPRPPSSRLPGIIGGYDORPTLPYVGDPITSSILPGGETPSQPPPLRP	480				
Db	421	TIFPYNPMLHPRPPSSRLPGIIGGYDORPTLPYVGDPITSSILPGGETPSQPPPLRP	480				
Qy	481	RFPDVGPLPGPNPILPGRGPNDRFPFRPGRGPRPTDGRLSFM	522				
Db	481	RFPDVGPLPGPNPILPGRGPNDRFPFRPGRGPRPTDGRLSFM	522				

RESULT 4

AD74366
 ID ADC74366 standard; protein; 522 AA.
 XX
 AC ADC74366;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Human secreted protein - SEQ ID 999.
 XX
 KW antianaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;
 KW antidabetic; immunosuppressive; dermatological; nephrotropic;
 KW antiparkinsonian; neuroprotective; nootropic; antibacterial; virucide;
 KW fungicide; antiparasitic; antiarteriosclerotic; vulnerary; cytostatic;
 KW haemopoietic; haematologic; anaemia; autoimmune disorder;
 KW rheumatoid arthritis; inflammation; Grave's disease; diabetes;
 KW systemic lupus erythematosus; glomerulonephritis; neurodegenerative;
 KW parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;
 KW cancer; bacterial; viral; fungal; parasitic infection; gene therapy;
 KW human.
 XX
 OS Homo sapiens.
 XX
 FN WO2003038063-A2.
 XX
 PD 08-MAY-2003.
 XX
 PF 19-MAR-2002; 2002WO-US008277.
 XX
 PR 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0331287P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 FI Rosen CA, Ruben SM;
 XX
 DR WPI; 2003-430516/40.
 DR N-PSDB; ADC73751.
 XX
 PT New human secreted polypeptide for diagnosing, preventing or treating
 PT hemopoietic or hematologic disorders (e.g. anemia), autoimmune
 PT disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or
 PT atherosclerosis).
 XX
 PS Claim 16; SEQ ID NO 999; 2272pp; English.
 XX
 CC The invention relates to a novel human secreted polypeptide comprising a
 CC defined sequence given in the specification. The polypeptide, nucleic
 CC acid molecule, antibody, agonist or antagonist of the invention may be
 CC useful for preparing a composition for diagnosing or treating a
 CC haemopoietic or haematologic disorder such as anaemia, autoimmune
 CC disorders such as rheumatoid arthritis, inflammation, Grave's disease,
 CC diabetes, systemic lupus erythematosus or glomerulonephritis,
 CC neurodegenerative disorders including Parkinson's disease and Alzheimer's
 CC disease, wounds and hyperproliferative disorders including
 CC atherosclerosis or cancer, as well as bacterial, viral, fungal or
 CC parasitic infections. The polypeptide may also be used during gene
 CC therapy procedures and for identifying a binding partner by contacting
 CC the polypeptide with a binding partner and determining whether the
 CC binding partner increases or decreases the activity of the polypeptide.
 CC The current sequence is that of the human secreted protein of the
 CC invention.
 XX
 SQ Sequence 522 AA;
 Query Match 99.8%; Score 2748; DB 7; Length 522;
 Best Local Similarity 99.8%; Pred. No. 6.5e-239;
 Matches 521; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MRLRVLLKRTWPLEVPEPTPLGLRSHLRSLCTWGYSSNTRFTITLNYKDLPTGDE 60
 DB 1 MRLRVLLKRTWPLEVPEPTPLGLRSHLRSLCTWGYSSNTRFTITLNYKDLPTGDE 60

61 ETLASYGIVSGDLICLILODDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNQTSMQDEQP 120
 |||||
 61 ETLASYGIVSGDLICLILODDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNQTSMQDEQP 120
 |||||
 121 SDSFGQAQSGVWDDSMGLGSPQNFESIQDQNAHMAEGTGFYSPBMLCSESVGEQVP 180
 |||||
 121 SDSFGQAQSGVWDDSMGLGSPQNFESIQDQNAHMAEGTGFYSPBMLCSESVGEQVP 180
 |||||
 181 HSLETLQSDADCSANDALIVLIHLLMESGYIPOGTEAKVLSMPKWKLSGVYKLYVMH 240
 |||||
 181 HSLETLQSDADCSANDALIVLIHLLMESGYIPOGTEAKVLSMPKWKLSGVYKLYVMH 240
 |||||
 241 PLCGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKELGENVANIYKD 300
 |||||
 241 PLCGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKELGENVANIYKD 300
 |||||
 301 LQKLSRLFKDQLVYPLLAFTQALNLPDVGVLVPLLELKLIRPRLLDVRSVLSAVCR 360
 |||||
 301 LQKLSRLFKDQLVYPLLAFTQALNLPDVGVLVPLLELKLIRPRLLDVRSVLSAVCR 360
 |||||
 361 DLFTASNDPILLRFLYLRDPRDNTVRVQDQDMKELYRKHQKESPKGREVMLLPSSTH 420
 |||||
 361 DLFTASNDPILLRFLYLRDPRDNTVRVQDQDMKELYRKHQKESPKGREVMLLPSSTH 420
 |||||
 421 TIIFYPNPLHPRPPFPSSRLPGIIGGYDQRTPLPYVGDPISSLIPOGETPSQFPPLRP 480
 |||||
 421 TIIFYPNPLHPRPPFPSSRLPGIIGGYDQRTPLPYVGDPISSLIPOGETPSQFPPLRP 480
 |||||
 481 RFDVGPGLPGNPILPGRGGNDPRFPRSRGRPTDGRLSPM 522
 |||||
 481 RFDVGPGLPGNPILPGRGGNDPRFPRSRGRPTDGRLSPM 522
 |||||

RESULT 5
 AAB35161
 ID AAB35161 standard; protein; 522 AA.
 XX
 AC AAB35161;
 XX
 DT 09-APR-2001 (first entry)
 XX
 DE Human Skpl-associated F-box protein-1 SAF-beta SEQ ID NO: 10.
 XX
 KW Human; protein degradation; siah-mediated degradation protein; SMDP;
 KW SCF-complex protein; SCP; siah-1alpha; siah-1 interacting protein; SIP;
 KW Skpl-associated F-box protein; SAF-1; SAF-2; SAD; cancer; cell division;
 KW Skpl-associated destruction-box protein; inflammatory disease.
 XX
 OS Homo sapiens.
 XX
 FN WO200077207-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 09-JUN-2000; 2000WO-US015873.
 XX
 PR 11-JUN-1999; 99US-00330517.
 XX
 PA (BURN-) BURNHAM INST.
 XX
 PI Reed JC, Matsuzawa S;
 XX
 DR WPI; 2001-071273/08.
 DR N-PSDB; AAC67285.
 XX
 PT Siah-Mediated Degradation Protein, useful for drug screening, for
 PT therapeutic applications and for functional genomics.
 XX
 PS Claim 15; Page 107-108; 121pp; English.
 XX
 CC The present invention provides the protein and coding sequences of
 CC several siah-mediated degradation proteins and SCF-complex proteins.
 CC These are designated Siah-1alpha, Siah-1 interacting protein (SIP), which

CC encodes two proteins due to alternative splicing (SIP-L and SIP-S), Skpl-
CC associated F-box protein-1alpha and beta and -2 (SAF-1alpha, SAF-1beta
CC and SAF-2) and Skpl-associated destruction-box protein (SAD). The
CC proteins and their coding sequences are useful in the diagnosis and
CC treatment of cancers, disorders where too little cell division occurs
CC such as bone marrow aplasia, immunodeficiencies and inflammatory
CC diseases including sepsis, fibrosis, arthritis and graft versus host
CC disease
XX
XX
SQ Sequence 522 AA;

Query Match 99.6%; Score 2744; DB 4; Length 522;
Best Local Similarity 99.6%; Pred. No. 1.5e-238;
Matches 520; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRLRVLLKRTWPLEVETPTGLHLSRLSLCTGWSSNTRFTITLYKDPPLTGE 60
DB 1 MRLRVLLKRTWPLEVETPTGLHLSRLSLCTGWSSNTRFTITLYKDPPLTGE 60
QY 61 ETLASYGIVSGDLICILQDDIPAPNIPSTDSHSLQNEQPSLATSSNQTSMDQEP 120
DB 61 ETLASYGIVSGDLICILQDDIPAPNIPSTDSHSLQNEQPSLATSSNQTSMDQEP 120
QY 121 SDSFQGAQSGVWDDSMGLPSONFEASTQDNAMHAEAGTGFYPSFPMCLSESVEGQVP 180
DB 121 SDSFQGAQSGVWDDSMGLPSONFEASTQDNAMHAEAGTGFYPSFPMCLSESVEGQVP 180
QY 181 HSLETLQSAQSDANDALIVLHLLMLESYIPQGTAEAKALSMPEKWLKSGVYKLYMH 240
DB 181 HSLETLQSAQSDANDALIVLHLLMLESYIPQGTAEAKALSMPEKWLKSGVYKLYMH 240
QY 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKEKLGENVANYKD 300
DB 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKEKLGENVANYKD 300
QY 301 LQKLSRLFKDQVYPLLAFTQALNLPDVGLVPLLEKLRIFRLLDVRSVLSAVCR 360
DB 301 LQKLSRLFKDQVYPLLAFTQALNLPDVGLVPLLEKLRIFRLLDVRSVLSAVCR 360
QY 361 DLFTASNDPPLLWFLYLRDRFNDTRVQDQDWKELYRKRIHQKESPKGRFVMLLPSSSTH 420
DB 361 DLFTASNDPPLLWFLYLRDRFNDTRVQDQDWKELYRKRIHQKESPKGRFVMLLPSSSTH 420
QY 421 TIFYPNPLHPPSPSSRLPGIIGGYDQRTPLPYVGDPISSLIPOGGETPSQFPPLRP 480
DB 421 TIFYPNPLHPPSPSSRLPGIIGGYDQRTPLPYVGDPISSLIPOGGETPSQFPPLRP 480
QY 481 RFDVGLPGNPILPGRGPNDRPFRPSGRGPTDGLRSLFM 522
DB 481 RFDVGLPGNPILPGRGPNDRPFRPSGRGPTDGLRSLFM 522

RESULT 6
ABM82342
ID ABM82342 standard; protein; 522 AA.
XX
AC ABM82342;
XX
DT 18-NOV-2004 (first entry)
XX
DE Tumour-associated antigenic target (TAT) polypeptide PR083271, SEQ:6018.
XX
KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2004030615-A2.

XX 15-APR-2004.
XX 29-SEP-2003; 2003WO-US028547.
XX 02-OCT-2002; 2002US-0414971P.
XX (GETH) GENENTECH INC.
XX Wu TD, Zhang Z, Zhou Y;
XX WPI; 2004-347921/32.
XX N-PSDB; ACN40919.
XX
XX New tumor-associated antigenic target polypeptides and nucleic acids,
XX useful in preparing a medicament for treating or detecting a
XX proliferative disorder, e.g. breast, lung, colorectal, ovarian or
XX prostate cancer or tumor.
XX
XX Claim 12; SEQ ID NO 6018; 7273pp; English.

CC The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention

SQ Sequence 522 AA;

Query Match 99.6%; Score 2744; DB 8; Length 522;
Best Local Similarity 99.6%; Pred. No. 1.5e-238;
Matches 520; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRLRVLLKRTWPLEVETPTGLHLSRLSLCTGWSSNTRFTITLYKDPPLTGE 60
DB 1 MRLRVLLKRTWPLEVETPTGLHLSRLSLCTGWSSNTRFTITLYKDPPLTGE 60
QY 61 ETLASYGIVSGDLICILQDDIPAPNIPSTDSHSLQNEQPSLATSSNQTSMDQEP 120
DB 61 ETLASYGIVSGDLICILQDDIPAPNIPSTDSHSLQNEQPSLATSSNQTSMDQEP 120
QY 121 SDSFQGAQSGVWDDSMGLPSONFEASTQDNAMHAEAGTGFYPSFPMCLSESVEGQVP 180
DB 121 SDSFQGAQSGVWDDSMGLPSONFEASTQDNAMHAEAGTGFYPSFPMCLSESVEGQVP 180
QY 181 HSLETLQSAQSDANDALIVLHLLMLESYIPQGTAEAKALSMPEKWLKSGVYKLYMH 240
DB 181 HSLETLQSAQSDANDALIVLHLLMLESYIPQGTAEAKALSMPEKWLKSGVYKLYMH 240
QY 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKEKLGENVANYKD 300
DB 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKEKLGENVANYKD 300
QY 301 LQKLSRLFKDQVYPLLAFTQALNLPDVGLVPLLEKLRIFRLLDVRSVLSAVCR 360
DB 301 LQKLSRLFKDQVYPLLAFTQALNLPDVGLVPLLEKLRIFRLLDVRSVLSAVCR 360
QY 361 DLFTASNDPPLLWFLYLRDRFNDTRVQDQDWKELYRKRIHQKESPKGRFVMLLPSSSTH 420

Db 361 DLFTASNDPLLRFLYLEDFRDNTVRVQDTWKELYRKRHIQRKESPKGRFVMLLPSSSTH 420
Qy 421 TIPYPNPLHPRPPSSRLPPIIGGYDQRTPLPYVGDPISSLIPIGGETPSQFPPLRP 480
Db 421 TIPYPNPLHPRPPSSRLPPIIGGYDQRTPLPYVGDPISSLIPIGGETPSQFPPLRP 480
Qy 481 RFDVPGLPGNPILPGRGGNDPRPPRPSRGRPTDGLRSPM 522
Db 481 RFDVPGLPGNPILPGRGGNDPRPPRPSRGRPTDGLRSPM 522

RESULT 7
ADU46626
ID ADU46626 standard; protein; 522 AA.

XX AC ADU46626;
XX DT 27-JAN-2005 (first entry)
XX DE Human Fbx7 protein sequence.

KW Fbx7; cancer; cyclin-D; proto oncogene; cdk6; cell cycle;
KW E3 ubiquitin ligase; SCF; F box; lung cancer; Fbx7 inhibitor;
KW colon cancer; hematological cancer; leukaemia; lymphoma; sarcoma;
KW carcinoma; adenocarcinoma; head and neck cancer; parathyroid adenoma;
KW oncoprotein; gene therapy; cytostatic; anti-cancer.
XX OS Homo sapiens.

XX FH Location/Qualifiers
FT Domain 129..169
FT /note = Non-contiguous domain in Fbx7. Known to interact
FT with cdk6
FT Region 335..372
FT /note= "F box motif"
FT Domain 398..522
FT /note = Non-contiguous domain in Fbx7. Known to interact
FT with cdk6
FT /label = Proline_Rich_domain
FT Region 406
FT /note= "Cyclin/cdk serine phosphodiester site"

XX WO2004093919-A2.
XX PD 04-NOV-2004.
XX PF 22-APR-2004; 2004WO-GB001743.
XX PR 22-APR-2003; 2003GB-00009116.

XX (UNLO) UNIV COLLEGE LONDON.

XX Laman H;
XX WPI; 2004-775870/76.
XX DR N-PSDB; ADU46625.

XX Use of an inhibitor of Fbx7 in the manufacture of a medicament for
XX treating cancer, such as lung cancer, colon cancer or a hematological
XX cancer, or in drug screening purposes.

XX Disclosure; SEQ ID NO 2; 69pp; English.

XX The patent discloses inhibitor of Fbx7 in the manufacture of a medicament
XX for use on the treatment of cancer. D-type cyclins are considered as
XX proto oncogenes, the over expression of these cyclins activates the G1
XX kinases, cdk4 and cdk6 proteins. These in turn activate the
XX retinoblastoma protein, permitting entry into the cell cycle. Fbx7
XX distinguishes between the G1 cdk6 and specifically enhances the levels of
XX cyclin/cdk6 complexes. The protein abundance in a cell is regulated both
XX at the level of rates of synthesis and of degradation. Poly-
XX ubiquitination mediated degradation is mediated via the E3 ubiquitin

CC ligases. The best characterised E3 activities include the anaphase-
CC promoting complex (APC), the HECT domain proteins, and the SCF complexes.
CC SCF E3 ubiquitin ligase, comprises of multiple subunits, including Skp1, a
CC cullin protein, a RING finger protein, and a F box motif, which binds the
CC skp1 subunit. In humans, two Fbx proteins skp2 and cdc4 have been
CC identified as being critical for the turnover of important cell cycle
CC regulators, p27, and cyclin E. It has been observed that cells engineered
CC to express Fbx7, become transformed, and exhibit phenotypes of a cancer
CC cell. Fbx7 over expression has been observed in lung cancer, colon cancer
CC and hematological cancers. Thus, Fbx7 is a novel oncoprotein which acts
CC by way of cyclins/cdk6. Thus Fbx inhibitors of the invention can be used
CC to treat cancers such as leukaemia, lymphoma, sarcoma, carcinoma,
CC adenocarcinoma, head and neck cancer, parathyroid adenoma. The invention
CC also related to a pharmaceutical composition comprising the Fbx7, for
CC treating a host suffering from cancer. The inhibitor may be a chemical
CC small molecule or can be an antisense RNA, inhibiting the Fbx7 expression
CC by RNA interference (RNAi). The objective of using the inhibitor would be
CC to, inhibit Fbx7 in the interaction between Fbx7 and a D-type cyclin
CC and/or cdk6 in the host. The sequence presented here is the human Fbx7
CC protein sequence.
XX Sequence 522 AA;

Qy Query Match 99.6%; Score 2744; DB 8; Length 522;
Db Best Local Similarity 99.6%; Pred. No. 1.5e-238;
Matches 520; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRLRVLLKRTWPLEVPEPETETLGLRSHLRSLCLLTGWYSSNTRFTITLNYKDLPTGDE 60
Db 1 MRLRVLLKRTWPLEVPEPETETLGLRSHLRSLCLLTGWYSSNTRFTITLNYKDLPTGDE 60
Qy 61 ETLASYGIVSGDLICLLIQLDDIPAPNIPSSSTDSEHSSIQNNEQPSLATSSNQTSMQDSQP 120
Db 61 ETLASYGIVSGDLICLLIQLDDIPAPNIPSSSTDSEHSSIQNNEQPSLATSSNQTSMQDSQP 120
Qy 121 SDSFQQAQSGVWVNDSDMLGPSQNFEAESIQDNNAHMAEGTFYSEPMLCSESVGEQVP 180
Db 121 SDSFQQAQSGVWVNDSDMLGPSQNFEAESIQDNNAHMAEGTFYSEPMLCSESVGEQVP 180
Qy 181 HSLETLQYQADCSANDALIVLIHLLMESGYIPQGTAKALSMPEKWKLSGVYKLOQYMH 240
Db 181 HSLETLQYQADCSANDALIVLIHLLMESGYIPQGTAKALSMPEKWKLSGVYKLOQYMH 240
Qy 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKELGENVANIYKD 300
Db 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKELGENVANIYKD 300
Qy 301 LQKLSRLFKDOLVYPLLAFTQALNLPDVFGVLVPLLELKLRIFRLLDVRSVLSAYCR 360
Db 301 LQKLSRLFKDOLVYPLLAFTQALNLPDVFGVLVPLLELKLRIFRLLDVRSVLSAYCR 360
Qy 361 DLFTASNDPLLRFLYLRDNRDNTVRVQDTWKELYRKRHIQRKESPKGRFVMLLPSSSTH 420
Db 361 DLFTASNDPLLRFLYLRDNRDNTVRVQDTWKELYRKRHIQRKESPKGRFVMLLPSSSTH 420
Qy 421 TIPYPNPLHPRPPSSRLPPIIGGYDQRTPLPYVGDPISSLIPIGGETPSQFPPLRP 480
Db 421 TIPYPNPLHPRPPSSRLPPIIGGYDQRTPLPYVGDPISSLIPIGGETPSQFPPLRP 480
Qy 481 RFDVPGLPGNPILPGRGGNDPRPPRPSRGRPTDGLRSPM 522
Db 481 RFDVPGLPGNPILPGRGGNDPRPPRPSRGRPTDGLRSPM 522

RESULT 8
ADZ70638
ID ADZ70638 standard; protein; 522 AA.

XX AC ADZ70638;

XX DT 30-JUN-2005 (first entry)

XX DE Human protein from lung cancer marker gene FBX07.

XX Tumor marker; lung tumor; cytostatic; neoplasm; expression;
KW DNA microarray.
XX
XX Homo sapiens.
XX WO2005032495-A2.
XX 14-APR-2005.
XX 01-OCT-2004; 2004WO-US034163.
XX 03-OCT-2003; 2003US-0508355P.
XX (FARB) BAYER PHARM CORP.
XX
XX Taylor I, Pauloski NR, Bigwood D;
XX WPI; 2005-285325/29.
XX N-PSDB; ADZ70637.
XX
XX Providing a patient diagnosis for lung cancer comprises comparing the
XX level of expression of genes or gene products in a biological sample from
XX the patient with that from a normal individual.
XX
XX Claim 3; SEQ ID NO 323; 60pp; English.
XX
XX The invention relates to providing a patient diagnosis for lung cancer
XX comprising comparing the level of expression of genes or gene products in
XX a biological sample from the patient with the level of expression of
XX genes or gene products in a biological sample from a normal individual.
XX Also included are distinguishing between normal and disease tissues,
XX monitoring the response of a patient being treated for lung cancer by
XX administering an anti-cancer agent, identifying a compound useful for the
XX treatment of lung cancer and an array for distinguishing between normal
XX and disease tissues (comprising 2 or more probes corresponding to 2 or
XX more genes selected from any of the 200 nucleotide sequences given in the
XX specification, or 2 or more polypeptides comprising any of the 200 amino
XX acid sequences given in the specification). In providing a patient
XX diagnosis for lung cancer, one or more genes are selected from any of the
XX 200 nucleotide sequences as mentioned in the specification, or one or
XX more gene products are polypeptides selected from any of the 20 amino
XX acid sequences mentioned in the specification. The methods are useful for
XX detecting and treating lung cancer. These may also be used for designing,
XX identifying and optimizing therapeutics for cancer. The present sequence
XX represents a protein from one of the 200 lung cancer marker genes. Note:
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 522 AA;
Query Match 99.6%; Score 2744; DB 9; Length 522;
Best Local Similarity 99.6%; Pred. No. 1.5e-238;
Matches 520; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLRLVRLKRTWPLEVETETPTLGLHSLRLSLCTWTGYSNNTRFTITLNYKDLPTGDE 60
DB 1 MLRLVRLKRTWPLEVETETPTLGLHSLRLSLCTWTGYSNNTRFTITLNYKDLPTGDE 60
QY 61 ETLASYGIVSGDLICLLIQDDIPAPNIPSTDSHSLQNNQPSLATSNQTSMDQEQP 120
DB 61 ETLASYGIVSGDLICLLIQDDIPAPNIPSTDSHSLQNNQPSLATSNQTSMDQEQP 120
QY 121 SDSFQGAAGVWDDSMGLPSONFEASIQDHAHAETGTFYPSPEMLCSSEVEQVP 180
DB 121 SDSFQGAAGVWDDSMGLPSONFEASIQDHAHAETGTFYPSPEMLCSSEVEQVP 180
QY 181 HSLTLYQSADCSANDALIVLHLLMLESYIPQGTAEAKALSMPEKWKLSGVYKQYMH 240
DB 181 HSLTLYQSADCSANDALIVLHLLMLESYIPQGTAEAKALSMPEKWKLSGVYKQYMH 240
QY 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKELGENVANIYKD 300

DB 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKELGENVANIYKD 300
QY 301 LOKLSRLPKDQLVYPLLAFTQALNLPDVGLVVLPLELKLRIEFLLDVRSVLSAVCR 360
DB 301 LOKLSRLPKDQLVYPLLAFTQALNLPDVGLVVLPLELKLRIEFLLDVRSVLSAVCR 360
QY 361 DLFTASNDPLLMRELYLRDFRDNTVRVQDQTDWKELYRKRHIQRKESPKGRFVMLLPSSSTH 420
DB 361 DLFTASNDPLLMRELYLRDFRDNTVRVQDQTDWKELYRKRHIQRKESPKGRFVMLLPSSSTH 420
QY 421 TIPIYPNPLHPRPPSSRLPPGIIGBYDORPTLPYVGDPDISSLIPOGETPSPQPPPLRP 480
DB 421 TIPIYPNPLHPRPPSSRLPPGIIGBYDORPTLPYVGDPDISSLIPOGETPSPQPPPLRP 480
QY 481 RFDVVGPLPGPNPILPGRGGPNDRFPFRPSRGRPTDGRLSFM 522
DB 481 RFDVVGPLPGPNPILPGRGGPNDRFPFRPSRGRPTDGRLSFM 522

RESULT 9

AAW68521
ID AAW68521 standard; protein; 591 AA.
XX
AC AAW68521;
XX
DT 25-JAN-1999 (first entry)
XX
DE Human RIP-associated protein.
XX
KW Human; RIP-associated protein; RAP; primer; PCR; amplification; probe;
KW hybridisation; death domain; MORT MODULE; ICE-like family protease;
KW kinase; TRAF domain; inflammation; cell death; tumour; HIV; infection.
XX
OS Homo sapiens.
XX
PN WO9841624-A1.
XX
PD 24-SEP-1998.
XX
PF 19-MAR-1998; 98WO-IL000125.
PR 19-MAR-1997; 97IL-00120485.
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Wallach D, Kovalenko A;
XX
DR WPI; 1998-531565/45.
DR N-PSDB; AAV57200.
XX
PT DNA encoding RIP-associated protein (RAP) - useful for, e.g. treatment of
PT tumour cells or HIV-infected cells.
XX
PS Claim 10; Fig 2; 65pp; English.
XX
CC This sequence represent part of a human RIP-associated protein (RAP). The
CC coding sequence was isolated from a B-cell library by a yeast 2-hybrid
CC screen using the RIP protein devoid of its "death domain" as a bait. The
CC screen isolated a clone of about 1.9 kb. Primers were generated based on
CC the sequence and used to PCR amplify probes for screening a colon and
CC heart cDNA library. A further 300 bp of sequence was determined, which
CC was added to the 1.9 kb of sequence from the B-cell library. The encoded
CC protein does not contain a "death domain", MORT MODULE, ICE-like family
CC protease domain, kinase domain, nor TRAF domains. RAP was shown to bind
CC only to RIP and not to TRADD, MORT-1, p55-R, p75-R or MACH. The protein
CC can be used to modulate or mediate RIP modulated/mediated intracellular
CC effects on the inflammation, cell death or cell survival pathways in
CC which RIP is involved, e.g. for treating tumour cells or HIV-infected
XX cells
SQ Sequence 591 AA;

Query Match	91.1%; Score 2510; DB 2; Length 591;	
Best Local Similarity	99.6%; Pred. No. 2.5e-217;	
Matches 479; Conservative 0; Mismatches 0; Indels 2; Gaps 1;		
Qy	42	SNTRFTITLNYKDPDGTGDEETLASYGIVSGDLICLIILQDDIPAPNIPSSSTDSEHSSLQNN 101
Db	113	SNTRFTITLNYKDPDGTGDEETLASYGIVSGDLICLIILQDDIPAPNIPSSSTDSEHSSLQNN 172
Qy	102	EQPSLATSSNOTSMODEQPSDFGQAAQSGVWDDSMLGPSQNFPEAESIQDNAMHAEAGT 161
Db	173	EQ--LATSSNOTSMODEQPSDFGQAAQSGVWDDSMLGPSQNFPEAESIQDNAMHAEAGT 230
Qy	162	GFYSEPMCLCSVEGQVPHSLFTLYQSADCSNDALIVLIHLMLSESGYIPQGTAKA 221
Db	231	GFYSEPMCLCSVEGQVPHSLFTLYQSADCSNDALIVLIHLMLSESGYIPQGTAKA 290
Qy	222	LSMPEKWKLSGVYKLYQVHPLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLP 281
Db	291	LSMPEKWKLSGVYKLYQVHPLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLP 350
Qy	282	ESFICKEKLGENVANIYKDLQKLSRLFKDQVYPLLAFTQALNLPDVFGVLVLPLELKL 341
Db	351	ESFICKEKLGENVANIYKDLQKLSRLFKDQVYPLLAFTQALNLPDVFGVLVLPLELKL 410
Qy	342	RIFRLDVRSLVLSAVCRDLFTASNDPDLWRFLYLRDRFRONTVRVQDWDKELYRKHHI 401
Db	411	RIFRLDVRSLVLSAVCRDLFTASNDPDLWRFLYLRDRFRONTVRVQDWDKELYRKHHI 470
Qy	402	QRKESPKGRFVWLLPSSSTHTTIPFPNPLHPRFPSSRLPPGIIGEYDQRTPLPVGDPI 461
Db	471	QRKESPKGRFVWLLPSSSTHTTIPFPNPLHPRFPSSRLPPGIIGEYDQRTPLPVGDPI 530
Qy	462	SSLIPGGETPSQFPPLRPDPVGPPLPGPNPILPGRGGPNDRPFRPSRGRPTDGRLSF 521
Db	531	SSLIPGGETPSQFPPLRPDPVGPPLPGPNPILPGRGGPNDRPFRPSRGRPTDGRLSF 590
Qy	522	M 522
Db	591	M 591
RESULT 10		
AA83047		
Id	AA83047	standard; protein; 482 AA.
XX	AC	AA83047;
XX	AC	AA83047;
DT	16-AUG-2000	(first entry)
XX	XX	F-box protein FBP-7.
DE	XX	F-box protein; FBP; diagnosis; treatment; screening; agonist; antagonist;
KW	XX	proliferative disorder; differentiative disorder; breast cancer;
KW	XX	prostate cancer; ovarian cancer; cancer; small cell lung carcinoma;
KW	XX	immune disorder; cardiovascular disorder; inflammatory disorder; human.
XX	OS	Homo sapiens.
XX	PN	WO200012679-A1.
XX	XX	09-MAR-2000.
XX	XX	27-AUG-1999; 99WO-US019560.
XX	XX	28-AUG-1998; 98US-0098355P.
PR	03-FEB-1999;	99US-0118568P.
PR	15-MAR-1999;	99US-0124449P.
XX	XX	(UNYV) UNIV NEW YORK STATE.
XX	PA	Chiaur DS, Pagano M, Latres E;
XX	PI	WPI; 2000-256635/22.
XX	XX	
DR	N-PSDB; AA293356.	
XX	Novel nucleic acid for screening compounds useful for treating	
PT	proliferative and differentiative disorders such as cancer and immune	
PT	disorders comprises sequences encoding ubiquitin ligases.	
XX	Claim 10; Fig 10a; 245pp; English.	
XX	Nucleic acids encoding substrate-targeting subunits of ubiquitin ligases	
CC	with F-box motifs (F-box proteins) are useful for diagnosis of	
CC	proliferative and differentiated related disorders by measuring FBP gene	
CC	expression. Cells expressing such proteins or their fragments are useful	
CC	for screening compounds. The compounds are agonists or antagonists, which	
CC	are useful for treating a proliferative or differentiative disorder in a	
CC	mammal such as breast, ovarian and prostate cancer and small cell lung	
CC	carcinoma and also major opportunistic infections, immune disorders,	
CC	cardiovascular diseases and inflammatory disorders. FBP protein, analogs,	
CC	derivatives and their subsequences, anti-FBP antibodies are also useful	
CC	in diagnosis of the disorders	
XX	Sequence 482 AA;	
Qy	Query Match 90.4%; Score 2489; DB 3; Length 482;	
Db	Best Local Similarity 98.1%; Pred. No. 1.5e-215;	
Qy	Matches 472; Conservative 5; Mismatches 4; Indels 0; Gaps 0;	
Db	42	SNTRFTITLNYKDPDGTGDEETLASYGIVSGDLICLIILQDDIPAPNIPSSSTDSEHSSLQNN 101
Qy	2	SNTRFTITLNYKDPDGTGDEETLASYGIVSGDLICLIILQDDIPAPNIPSSSTDSEHSSLQNN 61
Db	102	EQPSLATSSNOTSMODEQPSDFGQAAQSGVWDDSMLGPSQNFPEAESIQDNAMHAEAGT 161
Qy	62	EQPSLATSSNOTSIQDEQPSDFGQAAQSGVWDDSMLGPSQNFPEAESIQDNAMHAEAGT 121
Db	162	GFYSEPMCLCSVEGQVPHSLFTLYQSADCSNDALIVLIHLMLSESGYIPQGTAKA 221
Qy	122	GFYSEPMCLCSVEGQVPHSLFTLYQSADCSNDALIVLIHLMLSESGYIPQGTAKA 181
Db	222	LSMPEKWKLSGVYKLYQVHPLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLP 281
Qy	182	LSLPERKWKLSGVYKLYQVHPLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLP 241
Db	282	ESFICKEKLGENVANIYKDLQKLSRLFKDQVYPLLAFTQALNLPDVFGVLVLPLELKL 341
Qy	242	ESFICKEKLGENVANIYKDLQKLSRLFKDQVYPLLAFTQALNLPDVFGVLVLPLELKL 301
Db	342	RIFRLDVRSLVLSAVCRDLFTASNDPDLWRFLYLRDRFRONTVRVQDWDKELYRKHHI 401
Qy	302	RIFRLDVRSLVLSAVCRDLFTASNDPDLWRFLYLRDRFRONTVRVQDWDKELYRKHHI 361
Db	402	QRKESPKGRFVWLLPSSSTHTTIPFPNPLHPRFPSSRLPPGIIGEYDQRTPLPVGDPI 461
Qy	362	QRKESPKGRFVWLLPSSSTHTTIPFPNPLHPRFPSSRLPPGIIGEYDQRTPLPVGDPI 421
Db	462	SSLIPGGETPSQFPPLRPDPVGPPLPGPNPILPGRGGPNDRPFRPSRGRPTDGRLSF 521
Qy	422	SSLIPGGETPSQFPPLRPDPVGPPLPGPNPILPGRGGPNDRPFRPSRGRPTDGRLSF 481
Db	522	M 522
Qy	482	M 482
RESULT 11		
AAO22452		
Id	AAO22452	standard; protein; 482 AA.
XX	XX	AAO22452;
XX	XX	11-OCT-2002 (first entry)
XX	XX	Human F-box protein FBP7 SEQ ID No 14.

KW Cytostatic; immunomodulator; cardiant; antiinflammatory; antimicrobial;
KW proliferative; differentiative disorder; Skp2; F-box protein; cancer;
KW ubiquitin ligase; breast cancer; prostate cancer; ovarian cancer;
KW small lung carcinoma; immune disorder; parathyroid adenoma; FBP;
KW inflammatory disorder; lymphoma; major opportunistic infection;
KW certain cardiovascular disease; human.
XX
OS Homo sapiens.
XX
XX WO200255665-A2.
XX
XX 18-JUL-2002.
XX
XX 07-JAN-2002; 2002WO-US000311.
XX
XX 05-JAN-2001; 2001US-0260179P.
XX
XX (UYNY) UNIV NEW YORK STATE.
XX
XX Pagano M;
XX
XX WPI; 2002-599665/64.
XX
XX N-PSDB; AAL41047.
XX
XX Screening compounds for treating proliferative disorders, e.g. breast
PT cancer or prostate cancer, infections or immune disorders, comprises
PT detecting a change in the activity of Skp2 with either p27 or Cks1.
XX
XX
XX Disclosure; Fig 10; 246pp; English.
XX
XX The invention relates to screening compounds useful for the treatment of
CC proliferative or differentiative disorders comprising detecting a change
CC in the activity of Skp2 (F-box protein). The method is useful for
CC screening compounds for the treatment of proliferative or differentiative
CC disorders, particularly cancer. These compounds include small molecules,
CC or compounds or derivatives or analogues of the new ubiquitin ligases.
CC The compounds are useful for treating diseases such as cancer (e.g.
CC breast cancer, prostate cancer or ovarian cancer, lymphoma, small cell
CC lung carcinoma or parathyroid adenomas), major opportunistic infections,
CC immune disorders, certain cardiovascular diseases or inflammatory
CC disorders. This sequence represents an F-box protein (FBP) relating to
CC the invention
XX
XX Sequence 482 AA;
XX
Query Match 90.4%; Score 2489; DB 5; Length 482;
Best Local Similarity 98.1%; Pred. No. 1.5e-215;
Matches 472; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
Qy 42 SNTRFTITLNYKDPDTGDEETLASYGIVSGDLICLILQDDIPAPNIPSTDSHSSIQNN 101
Db 2 SNTRFTITLNYKDPDTGDEETLASYGIVSGDLICLILHDDIPPNIPSTDSHSSIQNN 61
Qy 102 EQPSLATSSNQTSMQDQPSDSFGQAAQSGVWVNDMSLQSPNFQAEISTQDHAHMAEGT 161
Db 62 EQPSLATSSNQTSDQPSDSFGQAAQSGVWVNDMSLQSPNFQAEISTQDHAHMAEGT 121
Qy 162 GFYPSEBMLCSVESGVPVSHLETLYQSADCSANDALIVLIHLMLSEGVIPQGTAKA 221
Db 122 GFYPSEBMLCSVESGVPVSHLETLYQSADCSANDALIVLIHLMLSEGVIPQGTAKA 181
Qy 222 LSPMEKWLKSGVKLQVMPHLCGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLP 281
Db 182 LSLPEKWLKSGVKLQVMPHLCGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLP 241
Qy 282 ESFICKEKLGENVANIYKDLQKLSRLPKDQLVPLLAFTQALNLPDVGVLVPLLEKL 341
Db 242 ESFICKEKLGENVANIYKDLQKLSRLPKDQLVPLLAFTQALNLPDVGVLVPLLEKL 301
Qy 342 RIFRLDVRVLSI-SAVCRDLFTASNDPLLRFLYLRDFRDNTRVQDTPWKELRKHI 401
Db 302 RIFRLDVRVLSI-SAVCRDLFTASNDPLLRFLYLRDFRDNTRVQDTPWKELRKHI 361

Qy 402 QRKESPKGRFVMLLPSTHTTIPYPNPLHRRPFPSSRLPPGIIIGGEYDQRTPLPYVGDP 461
Db 362 QRKESPKGRFVLLPSSHTTIPYPNPLHRRPFPSSRLPPGIIIGGEYDQRTPLPYVGDP 421
Qy 462 SSLIPGGETPSQFPPLPRFDPVGLPGGNPILPGRGGNDPFPSPSRGRTDGRLSF 521
Db 422 SSLIPGGETPSQFPPLPRFDPVGLPGGNPILPGRGGNDPFPSPSRGRTDGRLSF 481
Qy 522 M 522
Db 482 M 482
RESULT 12
ADY62371
ID ADY62371 standard; protein; 482 AA.
XX
XX AC ADY62371;
XX
XX 19-MAY-2005 (first entry)
XX
XX Human F-box protein, FBP7.
XX
XX screening; F-box protein; ubiquitin ligase; enzyme; diagnosis;
KW pharmaceutical; infertility; hyperproliferation;
KW differentiation disorder; cancer; infection; immune disorder;
KW cardiovascular disease; antiinfertility; cytostatic; cardiovascular-gen.;
KW antimicrobial; immunomodulator.
XX
XX Homo sapiens.
OS
XX
XX WO2005020922-A2.
XX
XX 10-MAR-2005.
XX
XX 27-AUG-2004; 2004WO-US028022.
XX
XX 28-AUG-2003; 2003US-00652928.
XX
XX (UYNY) UNIV NEW YORK STATE.
XX
XX Chiaur DS, Pagano M, Latres E;
XX
XX WPI; 2005-223081/23.
XX
XX N-PSDB; ADY62370.
XX
XX Screening compounds that modulate Fbp1 ubiquitin ligase-related
PT disorders, comprises contacting test compound with Fbp1 and Fbp5 and
PT measuring activity of Fbp1.
XX
XX Example; SEQ ID NO 14; 313pp; English.
XX
XX The invention relates to a method of screening (M1) compounds that
CC modulate F-box protein, FBP1 ubiquitin ligase-related disorders. The
CC method comprises contacting a test compound with FBP1 and FBP5, and
CC measuring the activity of FBP1, such that if the measured activity is
CC greater than or less than the activity measured in the absence of the
CC test compound, then a compound that modulates FBP1-related disorders is
CC identified. Optionally the method involves screening compounds useful for
CC the treatment of proliferative and differentiative disorder by contacting
CC a compound with a cell or a cell extract expressing both FBP1 and beta-
CC TRCP2, and an FBP1 target substrate, and detecting a change in the
CC activity of FBP1 or beta-TRCP2 or contacting a compound with a cell or a
CC cell extract expressing FBP1, and a test compound, and detecting a change
CC in the activity of FBP1, and contacting a compound with a cell or a cell
CC extract expressing beta-TRCP2, and a test compound, and detecting a
CC change in the activity of beta-TRCP2, and contacting a compound with a
CC cell or a cell extract expressing FBP1 and beta-TRCP2, and the test
CC compound or compounds identified as changing the activity of FBP1 or beta
CC -TRCP2, and detecting a change in the activity of FBP1 or beta-TRCP2.
CC Also described are: (1) a method of diagnosing (M2) decreased fertility
CC by examining FBP1 in infertile individuals by measuring the level of FBP1
CC expression or activity in a tissue sample from an affected individual,

and comparing the level of FBPI expression or activity in the affected individual with the level of FBPI expression or activity in a clinically normal individual, such that if decreased levels of FBPI expression or activity are detected in the affected individual relative to the clinically normal individual, an FBPI-related infertility disorder is diagnosed, (ii) a pharmaceutical composition for the treatment of FBPI-related infertility, comprising a compound that modulates FBPI activity and a carrier, (iii) a method of treating (M3) FBPI-related infertility by administering to an individual in the need of such treatment a compound that modulates FBPI activity, in an amount effective for the treatment of the infertility, and (iv) a method of detecting (M4) an FBPI infertility disorder in a mammal by measuring the level of FBPI activity or expression in the mammal, such that if the measured FBPI activity or expression differs from the level found in clinically normal individuals, then a FBPI-related infertility disorder is detected. Method (M1) is useful for screening compounds that modulate FBPI-related disorders and are useful for the treatment of proliferative and differentiative disorders. Method (M2) is useful for diagnosing decreased fertility by examining FBPI in infertile individual. A pharmaceutical composition comprising a compound that modulates FBPI activity and a carrier is useful for the treatment of FBPI-related infertility. Method (M3) is useful for treating FBPI-related infertility, and method (M4) is useful for detecting an FBPI-related infertility disorder in a mammal, preferably humans. The compounds screened by method (M1) are useful for treating infertility, cancer, major opportunistic infections, immune disorders, and certain cardiovascular disorders. This sequence represents a human F-box protein.

Sequence 482 AA;		Query Match	90.4%;	Score 2489;	DB 9;	Length 482;
Best Local Similarity		98.1%;	Pred. No. 1.5e-215;			
Matches 472;		Conservative	5;	Mismatches	4;	Indels 0; Gaps 0;
QY	42	SNTRFTITLNYKDPITGDEETLASVIGVSGDLICILQDDIPAPNIPSTDSHSSLQNN	101			
Db	2	SNTRFTITLNYKDPITGDEETLASVIGVSGDLICILHDDIPPPNIPSTDSHSSLQNN	61			
QY	102	EQPSLATSSNQTSMQDEPSDSFQCAQAQSGVWDDSLMGPSONFEASIQDNAHMAEGT	161			
Db	62	EQPSLATSSNQTSMQDEPSDSFQCAQAQSGVWDDSLMGPSONFEASIQDNAHMAEGT	121			
QY	162	GFYSEPMLCSESVGGVPHSLTLYQADCSANDALIVLIHLLMLESYGYPQCTEAKA	221			
Db	122	GFYSEPMLCSESVGGVPHSLTLYQADCSANDALIVLIHLLMLESYGYPQCTEAKA	181			
QY	222	LSMPEKWLKSGVYKLYQYHPLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLP	281			
Db	182	LSLPEKWLKSGVYKLYQYHPLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLP	241			
QY	282	ESFICKEKLGENVANIYKDLQKSLFKDQVYPLLAFTQALNLPDVFGLVVLELKL	341			
Db	242	ESFICKEKLGENVANIYKDLQKSLFKDQVYPLLAFTQALNLPDVFGLVVLELKL	301			
QY	342	RIFRLDDVRSVLSLAVCRDLFTASNDPLLRFLVLRDNTVRVQDQTDWKELRKXHI	401			
Db	302	RIFRLDDVRSVLSLAVCRDLFTASNDPLLRFLVLRDNTVRVQDQTDWKELRKXHI	361			
QY	402	QRKESPKGRFVMLLPSSTHTTIPFYNPLHPRFPSSRLPPGIIGEYDQRTPLPYVGDPPI	461			
Db	362	QRKESPKGRFVMLLPSSTHTTIPFYNPLHPRFPSSRLPPGIIGEYDQRTPLPYVGDPPI	421			
QY	462	SSLIPGQETPSQFPPLPRFPDVGPLPGPNILPGRGPNDRPFRPSRGRPTDGRLSF	521			
Db	422	SSLIPGQETPSQFPPLPRFPDVGPLPGPNILPGRGPNDRPFRPSRGRPTDGRLSF	481			
QY	522	M 522				
Db	482	M 482				

RESULT 13
AAU32109

ID	AAU32109	standard; protein; 607 AA.
XX	AC	AAU32109;
XX	DT	18-DEC-2001 (first entry)
XX	DE	Novel human secreted protein #2600.
XX	KW	Human; vaccination; gene therapy; nutritional supplement;
XX	KW	stem cell proliferation; haematopoiesis; nerve tissue regeneration;
XX	OS	immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX	PN	Homo sapiens.
XX	WO	WO200179449-A2.
XX	PD	25-OCT-2001.
XX	PF	16-APR-2001; 2001WO-US008656.
XX	PR	18-APR-2000; 2000US-00552929.
XX	PR	26-JAN-2001; 2001US-00770160.
XX	PA	(HYSE-) HYSEQ INC.
XX	PI	Tang YT, Liu C, Drmanac RT;
XX	WPI	2001-611725/70.
XX	PT	Nucleic acids encoding a range of human polypeptides, useful in genetic
XX	PT	vaccination, testing and therapy.
XX	PS	Claim 20; Page 556; 765pp; English.
XX	CC	The invention relates to novel human secreted polypeptides. The
XX	CC	polypeptides and antibodies to the polypeptides are useful for
XX	CC	determining the presence of or predisposition to a disease associated
XX	CC	with altered levels of polypeptide. The polypeptides are also useful for
XX	CC	identifying agents (agonists and antagonists) that bind to them. Calls
XX	CC	expressing the proteins are useful for identifying a therapeutic agent
XX	CC	for use in treatment of a pathology related to aberrant expression or
XX	CC	physiological interactions of the polypeptide. Vectors comprising the
XX	CC	nucleic acids encoding the polypeptides and cells genetically engineered
XX	CC	to express them are also useful for producing the proteins. The proteins
CC	are useful in genetic vaccination, testing and therapy, and can be used	
CC	as nutritional supplements. They may be used to increase stem cell	
CC	proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon	
CC	and/or nerve tissue growth or regeneration; immune suppression and/or	
CC	stimulation; as anti-inflammatory agents; and in treatment of leukaemias.	
CC	AAU29510-AAU33304 represent the amino acid sequences of novel human	
CC	secreted proteins of the invention	
XX	Sequence 607 AA;	
Query Match		88.9%; Score 2448.5; DB 4; Length 607;
Best Local Similarity		90.8%; Pred. No. 9.6e-212;
Matches 481;		Conservative 7; Mismatches 33; Indels 9; Gaps 5;
QY	1	MRLRVLLKRTWPLEVPEPTETLGHLSRLSLCTGWYSSNTRFTITLNYKDLTGDE 60
Db	36	MRLRVLLKRTWPLEVPEPTETLGHLSRLSLCTGWYSSNTRFTITLNYKDLTGDE 95
QY	61	ETLASVIGVSGDLICILQDDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNQTSMQDEQP 120
Db	96	ETLASVIGVSGDLICILQDDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNQTSMQDEQP 155
QY	121	SDSFGQAAQSGVWDDSLMGPSONFEASIQDNAHMAEGTFYSEPMLCSESVGGVQP 180
Db	156	SDSFGQAAQSGVWDDSLMGPSONFEASIQDNAHMAEGTFYSEPMLCSESVGGVQP 215
QY	181	HSLETLYQSADCSANDALIVLIHLLMLESYGYPQCTEAKALSMPEKWLKSGVYKLYMH 240
Db	216	HSLETLYQSADCSANDALIVLIHLLMLESYGYPQCTEAKALSMPEKWLKSGVYKLYMH 275

XX 27-DEC-2002.
PD 19-MAR-2002; 2002WO-US008278.
PF 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX (HUMA-) HUMAN GENOME SCI INC.
PA Rosen CA, Ruben SM;
XX WPI; 2003-167512/16.
FI N-PSDB; ADAS6693.
XX
DR New human secreted polypeptides and polynucleotides, useful for
PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
PT conditions, respiratory disorders, cancers, CNS disorders, or
PT neurodegenerative disorders.
XX
PS Claim 13; SEQ ID NO 1779; 1754pp; English.
XX
CC The invention relates to 592 new human secreted polypeptides useful for
CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
CC conditions, respiratory disorders, cancers, CNS disorders, or
CC neurodegenerative disorders, or polypeptides comprising an amino acid
CC sequence at least 95% identical to the new sequences. The polypeptides,
CC antibodies or antibody fragments that bind to the polypeptides, nucleic
CC acids encoding the polypeptides, agonists or antagonists that binds to
CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
CC compositions for diagnosing, treating or preventing an e.g. immune
CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
CC polynucleotides are useful for chromosome identification, chromosome
CC mapping, for controlling gene expression through triple helix formation
CC or antisense DNA or RNA, in gene therapy, for identifying individuals
CC from minute biological samples, in forensic biology, and as hybridization
CC probes. The polypeptides are useful for as molecular weight markers on
CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC gels, to raise antibodies, for testing biological activities, and for
CC treating or preventing neural disorders, immune system disorders,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal, proliferative and/or cancerous diseases. This sequence corresponds
CC to one of the polypeptide of the invention. Note: The sequence data for
CC this patent did form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 462 AA;

Query Match 87.3%; Score 2404; DB 6; Length 462;
Best Local Similarity 88.1%; Pred. No. 6.6e-208;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

QY 1 MRLRVLRLKRTWPLEVPETPTLGHRLSHRLSLCTWGYSSNTRFTITLNYKDPITGDE 60
DB 1 MRLRVLRLKRTWPLEVPETPTLGHRLSHRLSLCTWGYSSNTRFTITLNYKDPITGDE 60
QY 61 ETLASYGVSGDLICLIQDDIPAPNIPSSSTSEHSSIQNNQPSLATSSNOTSMQDEQP 120
DB 61 ETLASYGVSGDLICLIQDDIPAPNIPSSSTSEHSSIQNNQPSLATSSNOTSXQDEQP 120
QY 121 SDSFOGQAQSGVWDDSMGLPSONFEASIQDNAHMAEGTGYFSEPMLCSESVEGQVP 180
DB 121 SDSFOGQAQSGVWDDSMGLPSONFEASIQDNAHMAEGTGYFSEPMLCSESVEGQVP 180
QY 181 HSLETLYQSADCSANDALIVLIHLLMLESYIPQGTAKALSMPEKWLKSGVYKLQYMH 240

Db 181 HSLETLYQSADCSANDALIVLIHLLMLESYIPQGTAKALSMPEKWLKSGVYKLQYMH 240
QY 241 PLCEGSSATLTCVPLGNLIIVVNATLKINNEIRS VKRLQLLPESFICKELGENVANIYKD 300
Db 241 PLCEGSSATLTCVPLGNLIIVN-----
QY 301 LQKLSRLFKDQLVYVPLLAFTQALNLPDVGLVVLPLELKLRIIFRLLDVRSVLSAVCR 360
Db 263 -----ALNLPDVGLVVLPLELKLRIIFRLLDVRSVLSAVCR 300
QY 361 DLFTASNDPLLWRFLYLRDPRDNTVRVQDPTDWKELYRKRHIQRKESPKGRFVMLLPSSSTH 420
Db 301 DLFTASNDPLLWRFLYLRDPRDNTVRVQDPTDWKELYRKRHIQRKESPKGRFVMLLPSSSTH 360
QY 421 TIPFYPNPLHPRPFSSRLPGIIGGEYDQPTLPYVGDPISSLIIPGGETPSQPPPLRP 480
Db 361 TIPFYPNPLHPRPFSSRLPGIIGGEYDQPTLPYVGDPISSLIIPGGETPSQPPPLRP 420
QY 481 RFDVPVGPLPGPNPILPGRGGENDRFPFRPSRGRPTDGRLSFM 522
Db 421 RFDVPVGPLPGPNPILPGRGGENDRFPFRPSRGRPTDGRLSFM 462

Search completed: February 14, 2006, 20:57:47
Job time : 194 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 14, 2006, 20:58:08 ; Search time 41 Seconds
(without alignments)
1225.004 Million cell updates/sec

Title: US-09-927-458-2
Perfect score: 2754
Sequence: 1 MRLRVLLKRTWPLEVPETE.....DRFFRPSRGRPTDGLRSPM 522
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	240.5	8.7	475	2	A86372
2	187.5	6.8	350	2	H86371
3	145.5	5.3	547	2	T46366
4	128.5	4.7	842	2	T32558
5	118	4.3	564	2	H70804
6	117.5	4.3	1213	2	A41724
7	117	4.2	403	2	S52796
8	116.5	4.2	915	2	T12526
9	116	4.2	4957	2	T03455
10	116	4.2	5262	2	T03454
11	112	4.1	1006	2	G86292
12	111.5	4.0	940	2	JE0291
13	111	4.0	1097	2	T49187
14	110.5	4.0	551	2	S57447
15	110	4.0	424	2	A54964
16	110	4.0	1468	2	S11515
17	109.5	4.0	742	2	A49672
18	109.5	4.0	772	2	A55004
19	109	4.0	741	2	I48694
20	109	4.0	1206	2	S24407
21	109	4.0	2783	1	A41948
22	108	3.9	311	2	T15997
23	108	3.9	577	2	T09024
24	107.5	3.9	589	2	T29299
25	107	3.9	351	1	JSBYP1
26	107	3.9	505	2	A53152
27	107	3.9	1257	2	T01020
28	106.5	3.9	212	2	S57330
29	106.5	3.9	584	2	G71676

30	106	3.8	401	2	T51407	proline-rich prote
31	106	3.8	444	2	E83802	hypothetical prote
32	105.5	3.8	828	2	T06133	hypothetical prote
33	105.5	3.8	882	2	T43250	spindle pole body-
34	105.5	3.8	897	2	A39405	beta-galactosidase
35	105.5	3.8	1465	2	T23056	chromodomain helic
36	105	3.8	502	2	A55197	Wiskott-Aldrich sy
37	105	3.8	715	2	G86239	protein P20B24.6 (
38	104.5	3.8	235	2	A72594	hypothetical prote
39	104.5	3.8	301	2	JQ1663	hybrid proline-ric
40	104.5	3.8	850	2	JC5047	ras GTPase-activat
41	104	3.8	178	2	T36013	probable integral
42	104	3.8	188	2	D29149	proline-rich prote
43	104	3.8	574	2	H86467	probable transcrip
44	104	3.8	708	2	D96711	hypothetical prote
45	104	3.8	1252	2	D71810	probable type II D

ALIGNMENTS

RESULT 1

A86372

53.0K hypothetical protein F508.33 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: A86372

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federapfel, N.A.; Kaul, S.; White, O.; Alonac

ansen, N.F.; Hughes, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: A86372

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-475 <STO>

A:Cross-references: UNIPROT:Q9ZUB8; UNIPARC:UPI00000ACSB6; GB:AE005172; NID:G4056460; P

C:Genetics:

A:Map position: 1

Query Match 8.7%; Score 240.5; DB 2; Length 475;
Best Local Similarity 24.5%; Pred. No. 9.1e-10;
Matches 116; Conservative 89; Mismatches 177; Indels 91; Gaps 20;

QY	1	MRLRVLLKRTWPLEVPEPTGLHLSRLSLCTGWYSSNTRFTITLNYKDL--TG 58
DB	3	LRURHHTRETLKLEADAD-TLHURRRINPTV-----PSSVHLSLNRKDELTPS 53
QY	59	DEETLASYGIVSGDLCLILQDDIPAPNPSSDSEHSSLQNNNEQPSLATSSNQTQMODE 118
DB	54	PEDTLASGLISGLIVFSL-----ACESSNWKLRDSETVASQESQTSVHD- 102
QY	119	QPSDSFGQQAQSGVWDDSMGLQPSQNFEAESIQDNHMAEG--TGYPSPSPM----- 169
DB	103	--SIGP-----AEVDVVPDQAKSNPN-----TSVED-----PEGDISGMEGPEDVEQLDM 147
QY	170	--LCSESVESQVPHSLLET--LYQADCSDDANDALIVLHLLMLESGVI--PGQTE----- 218
DB	148	ELAAAGSKRLSEPFPLKNILLESKGTSELT-TLALSVHVMLESGLVNLHSGDKNFNS 206
QY	219	AKALSMPEKWLKSGVYKQLQYMHPLCEGSSATLTCVPLGNLIVVNATL-----KINNEI-- 271
DB	207	KELLTVSLRYTLPELIKSKDNTI---ESVSVKFQNLGPVVVVVGTGGSSGRVHMLDK 263
QY	272	-RSVKRLQLLPESFICEKELGENVANIYKDLQKLKRLFKDQLVYPLLAFTRAQLNLPDVF 330
DB	264	RRFPVPIDLVMDTSTDE---EGSSSYREVFMVFMVKDRLVIPLLLIGICDKAGLEPPP 320

Qy 331 GLVVLPLELKLRIFFLLDVRSLVLSAYCRDLFTASNDPLLRFLYLRFRDNTVRV--Q 388
Db 321 CLMLPTELKLELLELPGVSGNMACVCTEMRYLASNDLWKQCLSEVNFVVTAGD 380
Qy 389 DTDWK-----ELYRKRIHQRKESPKGRFVWMLLPSSHTTIPF 424
Db 381 SVNKKARFATWRQKLAASDTPFRQNLGRNISTGRSGIRPFIIGDPPF 433
RESULT 2
H86371
40.0K hypothetical protein F508.32 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: H86371
R:Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.B.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H86371
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-350 <STO>
A:Cross-references: UNIPROT:Q9ZUB9; UNIPARC:UPI00000A3C19; GB:AE005172; NID:g4056459; P1
C:Genetics:
A:Map position: 1
Query Match 6.8%; Score 187.5; DB 2; Length 350;
Best Local Similarity 24.4%; Pred. No. 4.2e-06;
Matches 90; Conservative 58; Mismatches 118; Indels 103; Gaps 17;
Qy 172 SESVEGVQVHLE-----TLYOSADCSANDALIVLHLLMESGYI 213
Db 22 NSGIEGPVMDVELAAAKSKRLSEPFLLKNVLLKSGDTSOLT-ALALSVAHVMLESGFV 80
Qy 214 --PGTE-----AKALSMPEKWLKSGVYKLYMHPLCEGSSATLTCVPLGNLVNATL- 265
Db 81 LLDHGSDFKFSKLLSVSLRYTLPELITRKDNTV---ESVTVRFQNGPRLVYVYGTG 137
Qy 266 ---KINNEIRSVKRLQLLPESFICEKL---GENVANIYKDLQKSLFKDQVYPLLA 318
Db 138 GSCKEVH--WTSLSKSRFLPVIDLVDTLKFEKQSSSYREVFLMWKVDLVIPLL- 194
Qy 319 FTRQALNLPDVF-----LVVLPLELKLRIFFLLDVRSLVLSAYCRDLFTASNDPLLM 372
Db 195 -----IGLCDRAGLESPCLMLLPTELKLELLELPGVSGVIGYMACVCTEMRYLASNDLW 249
Qy 373 RFLYLRDNRDNTVRVQ--DWDKELY-----RKR--HQRKESPKGRFVWMLLPSSHTTIP 423
Db 250 EHKCLEGKGLWKLYGTGDVMDKRFASFARRRKLDLLARRNPPIKK----- 296
Qy 424 FVPNPLHRPPFPSSLLPPGIIGGEDQRPITLPYVGDPISSLIPGPGETPSQPPL- 478
Db 297 --SNRPFITLFPDR-----DRREPFRFG-----PSDFYRFLGLRDP 331
Qy 479 RPRFDVGP 487
Db 332 RDRFGFRDP 340
RESULT 3
T46366
hypothetical protein DKFZp434C0118.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C:Accession: T46366
R:Ottewaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23031
A:Accession: T46366
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-547 <AAA>
A:Cross-references: UNIPROT:Q9NT57; UNIPARC:UPI000007107F; EMBL:AL1137520
A:Experimental source: adult testis; clone DKFZp434C0118
C:Genetics:
A:Note: DKFZp434C0118.1

Query Match 5.3%; Score 145.5; DB 2; Length 547;
Best Local Similarity 21.7%; Pred. No. 0.0094;
Matches 98; Conservative 61; Mismatches 123; Indels 169; Gaps 24;
Qy 105 SLATSSNQTSMDQPSDSFQQAQAGVNMDDSMLG-PSQNFAESIQDNAHMAEGTGF 163
Db 72 SAAETGSRHPDTQHPSS--GGRCRGTESPSAAAGRPASMAEAE---EDCH----- 119
Qy 164 YPSEPMLCSESVGEQVPHSLETLVQSADCSANDALIVLHLLMESGYIIPQGTAKA-L 222
Db 120 -----SDTVR-----ADDDSENES-----PAETDLQAO 143
Qy 223 SMPEKWLKSGVYKLYMHPLCEG--SSATLTCVPL---GNLIVNATLKINNE----- 270
Db 144 QM-----FRAQWMPFELAPGVSSNLENRNCRAARGLQKTSADTKGQEQKESKA 194
Qy 271 ----IRSV-----KRLQLLPE-----SFICEKLGLENVANIY---KDLQ 302
Db 195 RELFLKAVEEQNGALYEAIFKYYRAMQLVPDIEFKITYTTRSPDGDGVGNSIEDNDDDS 254
Qy 303 KLSRL----FKDQLVYPLLAFTTRQALNL--PDV-----FGLVVLPLELKLRIFFL- 348
Db 255 KWADLLSYFOQ-----LTFQESVLKLCQPELESSQIHISVLPMEVLMIYIFRWVVSDDL 309
Qy 349 VRSVLISAVCRDLFTASNDPLLRFLYLRFRDNTVR-VQDWDKELYRKRHIQRKESP 407
Db 310 LRSLEQLSLVCRGYICARDPEIWRLLACKLVWGRSCIKLVYTTSWRENFLE- 362
Qy 408 KGRFVMLLPSS-----HTIPYFNPPLHRPPFPSSRLPGIIGGEYDQ 450
Db 363 RVREDGVVISKTTVIRQGEQSLDGFYRAWHQVEYI---RYIRFFPDGHV----- 408
Qy 451 RPTLPYVGDPISSLIPGPGETPSQPPLRPR 481
Db 409 -----MMLTTPPEPQSIVPRLRTR 427

RESULT 4

T32258
hypothetical protein C24A1.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C:Accession: T32258

R:Connell, M.

submitted to the EMBL Data Library, September 1997

A:Description: The sequence of C. elegans cosmid C24A1.

A:Reference number: Z21141

A:Accession: T32258

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-842 <CON>

A:Cross-references: UNIPROT:O17055; UNIPARC:UPI000017B7AE; EMBL:AF024491; PIDN:AAB70312.

A:Experimental source: strain Bristol N2; clone C24A1

C:Genetics:

A:Gene: CESP:C24A1.3

A:Map position: 3

A:introns: 43/2; 189/3; 234/1; 351/1; 511/3; 578/3; 594/2; 636/2; 675/3

Query Match 4.7%; Score 128.5; DB 2; Length 842;

Best Local Similarity 20.3%; Pred. No. 0.31;


```
Qy 467 -----GPGETSQF---PPLRRP-----DPVGLPGNPILPGEGGNDPFRPPSRGR 513
Db 685 PPLPTGPTSVTHFAFGPPLPQLSEGCGRDFOAPAPPAPPLPGLGPPVP--PPLPGSGL 742
Qy 514 P 514
Db 743 P 743

RESULT 7
S52796
prpL2 protein - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-May-1995 #sequence_revision 10-Nov-1995 #text_change 10-Sep-1997
C:Accession: S52796
R:Ruhlmann, A.; Kreideweiss, S.; Nordheim, A.
submitted to the EMBL Data Library, March 1995
A:Reference number: S52796
A:Accession: S52796
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-403 <RUH>
A:Cross-references: UNIPARC:UPI000017C32C; EMBL:X86019; NID:g762950; PID:g762951

Query Match 4.2%; Score 117; DB 2; Length 403;
Best Local Similarity 32.9%; Pred. No. 0.72;
Matches 46; Conservative 9; Mismatches 41; Indels 44; Gaps 9;

Qy 415 LPSSTHTTPFVNPILHPPFPSSR-----LPGGIIGVYDQRPTLPYVGDPISSL---IP 466
Db 203 VPSFTR--PSAPHRHLRPPPSRGPPLPPSSGN--DETPLPQRLNLSSTTPPLP 258
Qy 467 GPGET-----PSQFPLRFRFD-.-VGPLFGNPPI-----LPG----- 497
Db 259 SPGRSGPLPPVPVSRPPPPVDRDPGRSGPLPPPPPPVSRNGSTSRALPATQLPSPRGVD 318
Qy 498 --RGGPNDRF--PFRPSRGRP 514
Db 319 SPRSGPRPLPPDRPSAGAP 338

RESULT 8
T12526
hypothetical protein DKFp434M183.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C:Accession: T12526
R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z17524
A:Accession: T12526
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-915 <WAM>
A:Cross-references: UNIPROT:Q9Y4Q8; UNIPARC:UPI0000070795; EMBL:AL080141
A:Experimental source: adult testis; clone DKFp434M183
C:Genetics:
A:Note: DKFp434M183.1

Query Match 4.2%; Score 116.5; DB 2; Length 915;
Best Local Similarity 20.7%; Pred. No. 2.6;
Matches 129; Conservative 76; Mismatches 208; Indels 209; Gaps 36;

Qy 34 LLCTWGYSSNTRFTITLNV-KDPLTGDDETLASYGIVSGDLICLLIQDDIPAPNIPSTD 92
Db 205 LKVTLEQSRMKFLKLGYSKDEL---QKVKATW-----LKSDV---GLGESFPQ 247
Qy 93 SEHSSLQNEQPSLATSNQTSMDQEPDSFQGAQSGV--W-----NDDSM----- 139
Db 248 PKGNDLNSDRQAFCSQASKHTKEASAFDELVPQNTWPWEIPITKIDIGLLSQAL 307
Qy 140 ----LGPSON--FEAESIQDNAHMAEGTGF----YPSBMLCSVESGEQVPHSLTILYQS 189
```

```
Db 308 LLGLGFAVELCLKEERFADAIILAQAGDTLLKQTOERYLAKKKT--KISSLLACVVQK 365
Qy 190 -----ADCSAN--DALIVLIHLLMESGYIPOGTAKALSMPEKWKLSGVYKLYQWHP 241
Db 366 NWKDVVCTCSLKWREALALITY-----SGTE-----KFPFLCDMLTRMEQ----- 408
Qy 242 LCEGSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICK--EKLGENVANIY 298
Db 409 --EGSRA-----LTSEARL-----CYVCSGSVERLVECAKCH 439
Qy 299 KDLQKLSRLFKDQLVYPLLAFTQALNLPDVFGLVVLPLELKLRIFRLLDVRSVL----- 353
Db 440 ---QALSPMALQDLMEKVMVNLRSLEQLRGPHGVSPGP-----ATTYRVQYANLLAAQGS 492
Qy 354 ---SLSAVCRD-----LFTASNDPPLLNR-----FLYLRDFRDNTRVQDTHKE 394
Db 493 LATAMSLPRDCAQPPVQQLRDLFHAQGSVAVLQQSQPPFPFPRIVVGVTILHSETSSYR 552
Qy 395 L-YRKRHIQKESPKGRFVMLLPSSHTTIPYPNPLHPRPPSSR----- 438
Db 553 LGSQFSHQVTPSPRPR--VFTPOSSPAMPLAPS--HPSPYQGGRTQNISYRAGPQAI 608
Qy 439 ---LPPCI-----IGGEYDQRP-----TLPVVGDPPISSLIPG---PG-----E 470
Db 609 QPLPLSGVRPASSQPQLLGGQVQVQVNPVPGFPGTWPPLPGSPLPWACPGIMRPGSTSLPE 668
Qy 471 TPSQFP--PLRP-----RPDPVGPLPGNPILPG-----RGGND 503
Db 669 TPLRFLPLPLRPLPGFRMVSHTPAPPASFVPVYLPFGDPGAPCASSVLPTTGILTPHPGPD 728
Qy 504 RFPFRPS-RGRPTDGL--SPM 522
Db 729 SWKEAPAPRGNLQRNKLPTETFM 750

RESULT 9
T03455
ALR protein - human
C:Species: Homo sapiens (man)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C:Accession: T03455
R:Prasad, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.; Yano,
Oncogene 15, 549-560, 1997
A:Title: Structure and expression pattern of human ALR, a novel gene with strong homolog
A:Reference number: Z14954; MUID:97388474; PMID:9247308
A:Accession: T03455
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-4957 <PRA>
A:Cross-references: UNIPROT:O14686; UNIPARC:UPI00001100F1; EMBL:AF010404; NID:g2358286;
C:Genetics:
A:Gene: ALR
A:Map position: 12
C:Superfamily: acute lymphoblastic leukemia protein, ALR type
C:Keywords: alternative splicing

Query Match 4.2%; Score 116; DB 2; Length 4957;
Best Local Similarity 20.0%; Pred. No. 35;
Matches 102; Conservative 64; Mismatches 181; Indels 164; Gaps 25;

Qy 94 EHSSLQNEQPSLATSNQTSMDQEPDSFQGAQSGV--GVMNDD-SMLGPSQNFSAES 150
Db 3356 QQQQLQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 3409
Qy 151 IQDNAHMAEGTGFVPSEPM-----LCSESV----- 176
Db 3410 -QQQQQVALFGCM-PAPLQHFSSPGALGPTLLLTGKEQNTVDPAVSSEATEGSPSTHGG 3467
Qy 177 ---GQVPHSLTILYQSADCSANDALIVLIHLLMESGYIPQ-GTEAKALSMPEKWKLS 231
Db 3468 PLAIGTTPESMATEPGEVKPSLSGDSQLLVQ-----PQPOPQPSLSQLQPLPLRP 3518
```


Qy 424 FYPNPLHPPSPSLRPLPGIIGGYDQRPPTLPYVGDPISSILPGGETPSPQFPPLRPFD 483
Db 643 FPPGFGGMPGPHGG-PGGPVGPRLLGPPPPRPGDPPFDW---GGD-PMRGPMRG--- 694
Qy 484 PVGLPGNPILPGRGG-----PNDRPFPPPSR-----GRPTDGR 518
Db 695 --GPGFGPVHRRGGRGNGNEPPPPPPPPFRGARGSGSGGPPNGR 738
RESULT 13
T49187
hypothetical protein MAA21.90 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C:Accession: T49187
R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, K.
submitted to the Protein Sequence Database, April 2000
A:Reference number: 225018
A:Accession: T49187
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1097 <RIE>
A:Cross-references: UNIPROT:Q9LY69; UNIPARC:UPI00000A03E7; EMBL:AL1163818; GSPDB:GNO0061;
A:Experimental source: cultivar Columbia; BAC clone MAA21
C:Genetics:
A:Gene: ATSP:MAA21.90
A:Map position: 3
A:Introns: 106/2; 124/3; 165/3; 198/1; 210/2; 245/3; 265/1; 297/3; 337/3; 352/1; 394/1;
Query Match 4.0%; Score 111; DB 2; Length 1097;
Best Local Similarity 20.2%; Pred. No. 8.7;
Matches 111; Conservative 75; Mismatches 218; Indels 146; Gaps 26;
Qy 37 TWGY-----SSNTRFTITLYKOPLTGDETLASGYVSGDLICLILODD-IPAPN 86
Db 435 TWGLLKIMFEEGSTRKLSHLGFTLPVAEKQAVDG---LSSDLNGIRLEDTAADALD 491
Qy 87 IPSSTDSHSLQNEQ-----PSLATSSNOTSMODEPSD---SFQGAQAQSGVWNDD 138
Db 492 LDDSENAFAFANGDEGFNNFPAPKPTPVSTSAKDFMPSDTDFSTKGEETQEMOESEE 551
Qy 139 MLGP-----SQNFAESIQDN---AHMAEGTGFPYS--EPMLCSSES 174
Db 552 SSDPVFDNAIORALIVGYKRAVDQCITANKMADALVIAVG-GTALWESTREKLYKTSS 610
Qy 175 -----VEGVPHSLTLYQADCSDDANDALIVLIHLLMLSEGYIPQGTAKALSMPEKW 228
Db 611 APYMKVVSAMVNNDLRSLLIYTRSHKFWKETLALLC-----TFAQGEQW 653
Qy 229 KLSGVYKLYQWHPICEGSSATLTCVPLGN-LIVVNATLKINNEIRSVKRLQLLPESFCK 287
Db 654 T-----TLCDALASKL--MAAGNTLAAVLCYICAGNVDRIVE-----IWSRSLAN 696
Qy 288 EKLGENVANIYKOLQLKLSRLFKQQLVYPLA-----FTRQALNLPDVFGVLVLP---LELK 340
Db 697 ERDGRSYAELLQDLMEKT-----LVLATGNTKKFESASLCKLFESYAEILASQGLLTTA 750
Qy 341 LRIFRLLD-----VRSVLSISAVCRDLFTAS-----NDPLLMLRFLYL 378
Db 751 MKYLVLDGGLSPSLSLRDLRISABETNTTASGNTQPOSTWPNYQEFQAQPNVLA 810
Qy 379 DFRONTVRVQDMDWKELYRKRIQKESPKGRFVMLPSSHTIIP-----FYPNPLHPPFP 435
Db 811 NPYDNQYQOQVYDSYVYVQVSH-----PDMQOQTFMFMHQAQAPQPSFTPAPT--SNAQP 864
Qy 436 SSR-----LPGLIGGYDQRPPTLPYVGDPISSILPGGETPSPQFPPLRPFDVGPL- 488
Db 865 SMRTTFVSTPPALKNADQYOQFTWS-----SHSFTGPSNNAYVPVPPGQYAPSGPSQ 918
Qy 489 --PGNPILP 496
Db 919 LGQYFNPKM 928

RESULT 14

S57447
HPBRII-7 protein - human
N:Alternate names: HPBRII-4 protein
C:Species: Homo sapiens (man)
C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 05-Oct-2004
C:Accession: S57447; S57489
R:Fleischhauer, K.L.
submitted to the EMBL Data Library, June 1992
A:Reference number: S57447
A:Accession: S57447
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-551 <FILE>
A:Cross-references: UNIPROT:Q16630; UNIPARC:UPI000006D566; EMBL:X67336; NID:g871300; PID:9871300;
A:Accession: S57489
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-551 <FL2>
A:Cross-references: UNIPARC:UPI000006D566; EMBL:X67337; NID:g871298; PID:CAA47752.1; PID:9871300;
C:Genetics:
A:Introns: 231/3
F:82-151/Domain: ribonucleoprotein repeat homology <RRM4>
Query Match 4.0%; Score 110.5; DB 2; Length 551;
Best Local Similarity 31.1%; Pred. No. 3.4;
Matches 41; Conservative 9; Mismatches 39; Indels 43; Gaps 8;
Qy 408 KGRFVMLLPSSSTHTIPFVNPPL----HPRPPSSRLPPIIGGYDQRPPTLPYVGDPISS 463
Db 204 KGRFPAGVPGDGR----FPGPAGGPPPPPPACQTTP-----RPLGPGGPPGPP 250
Qy 464 LIPGFGET---PSQFPPLR-----PRFDPVGPL-PGPNPILPGRGPN 502
Db 251 GPPPPGGVLPPLAGPPNRRGDRPPPPVLPFGQPFQGP---PLGLPLPPGPPPPVPGYGPPP 307
Qy 503 DRFPFRPSRGRP 514
Db 308 G--PPPPQQGPP 317
RESULT 15
A54984
spliceosome-associated protein SAP-49 - human
C:Species: Homo sapiens (man)
C:Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 31-Dec-2004
C:Accession: A54984
R:Champion-Arnaud, P.; Reed, R.
Genes Dev. 8, 1974-1983, 1994
A:Title: The prespliceosome components SAP 49 and SAP 145 interact in a complex implicat
A:Reference number: A54964; MUID:95047348; PMID:7959871
A:Accession: A54964
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-424 <CHA>
A:Cross-references: UNIPROT:Q15427; UNIPARC:UPI0000135472; GB:L35013; NID:g556216; PID:n
F:14-81/Domain: ribonucleoprotein repeat homology <RRM4>
F:101-169/Domain: ribonucleoprotein repeat homology <RRM2>

Query Match 4.0%; Score 110; DB 2; Length 424;
Best Local Similarity 32.0%; Pred. No. 2.5;
Matches 39; Conservative 9; Mismatches 32; Indels 42; Gaps 9;
Qy 430 HPRPPSSRLP-PGI-----IG-----GEYDQRPPTLPYVGDPISSILP 469
Db 292 HPHPFPFGMPPHPCMSQMLAHGHGPHAGPGSGGQPPPPPPPG-----MPHPG 345
Qy 470 ETPSQFPLPRPF-DPV---GFLP-----GNPILPGRG--GPNDRFPFRSRG-----R 513
Db 346 PPMGMGPRGPPFGSPMGHPGMPPHGMGRGPPPLMPHPHGYTGPPRPYPYGYQRGLPPPR 405

Qy 514 PT 515
||
Db 406 PT 407

Search completed: February 14, 2006, 21:02:34
Job time : 46 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 14, 2006, 21:13:14 ; Search time 168 Seconds
(without alignments)
1298.255 Million cell updates/sec

Title: US-09-927-458-2
Perfect score: 2754
Sequence: 1 MLRLVRLKRTWPLEVPETE.....DRPFPRSGRGTGRLSFM 522

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2754	100.0	522	3	US-09-927-458-2
2	2754	100.0	522	4	US-10-245-593-2
3	2744	99.6	522	4	US-10-679-246-10
4	2489	90.4	482	4	US-10-042-417-14
5	2489	90.4	482	5	US-10-652-928-14
6	2489	90.4	482	6	US-11-073-485-14
7	2489	90.4	482	6	US-11-073-470-14
8	2404	87.3	462	3	US-09-397-945-200
9	2404	87.3	462	4	US-10-264-237-2485
10	2404	87.3	462	4	US-10-653-595-200
11	2404	87.3	497	3	US-09-397-945-435
12	2404	87.3	497	4	US-10-653-595-435
13	2270	82.4	443	4	US-10-679-246-8
14	2086.5	75.8	549	5	US-10-450-763-48869
15	1527	55.4	317	4	US-10-264-237-2484
16	1238	45.0	231	4	US-10-408-765A-752
17	1086	39.4	221	4	US-10-094-749-1723
18	714	25.9	174	3	US-09-397-945-434
19	714	25.9	174	4	US-10-653-595-209
20	714	25.9	174	4	US-10-653-595-434
21	714	25.9	175	3	US-09-397-945-209
22	396	14.4	76	4	US-10-029-386-27908
23	299	10.9	113	5	US-10-820-474A-133
24	265.5	9.6	225	5	US-10-450-763-37197
25	264.5	9.6	53	5	US-10-450-763-48868
26	249	9.0	47	4	US-10-029-386-33496
27	215.5	7.8	500	5	US-10-739-930-9910

28	211	7.7	485	4	US-10-425-114-59910	Sequence 59910, A
29	207	7.5	485	4	US-10-425-114-59131	Sequence 59131, A
30	201	7.3	485	4	US-10-425-114-60984	Sequence 60984, A
31	198	7.2	447	4	US-10-425-115-349540	Sequence 349540,
32	194	7.0	39	4	US-10-042-417-21	Sequence 21, Appl
33	194	7.0	39	5	US-10-652-928-21	Sequence 21, Appl
34	194	7.0	39	6	US-11-073-485-21	Sequence 21, Appl
35	194	7.0	39	6	US-11-073-470-21	Sequence 21, Appl
36	189	6.9	38	3	US-09-801-348-47	Sequence 47, Appl
37	164	6.0	38	3	US-09-801-348-49	Sequence 49, Appl
38	147	5.3	270	6	US-11-097-143-19197	Sequence 19197, A
39	144	5.2	408	4	US-10-284-237-1835	Sequence 1835, Ap
40	142	5.2	1131	4	US-10-425-115-355048	Sequence 355048,
41	140	5.1	379	4	US-10-264-049-2807	Sequence 2807, Ap
42	139	5.0	327	4	US-10-042-417-58	Sequence 58, Appl
43	139	5.0	327	4	US-10-679-246-12	Sequence 12, Appl
44	139	5.0	327	5	US-10-652-928-58	Sequence 58, Appl
45	139	5.0	327	6	US-11-073-485-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1

US-09-927-458-2
; Sequence 2, Application US/09927458
; Patent No. US20020058024A1
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNG/NGF RECEPTOR
; TITLE OF INVENTION: AND OTHER PROTEINS
; FILE REFERENCE: WALLACH=22A
; CURRENT APPLICATION NUMBER: US/09/927,458
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/IL98/00125
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: IL 120485
; PRIOR FILING DATE: 1997-03-19
; PRIOR APPLICATION NUMBER: 09/381,358
; PRIOR FILING DATE: 1999-09-20
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-927-458-2

Query Match 100.0%; Score 2754; DB 3; Length 522;
Best Local Similarity 100.0%; Pred. No 2.6e-223; Indels 0; Gaps 0;
Matches 522; Conservative 0; Mismatches 0

Qy	1	MLRLVRLKRTWPLEVPETEPTGLHRLSHRLSLCTGWYSSNTRFTITLNYKDLTGDE	60
Db	1	MLRLVRLKRTWPLEVPETEPTGLHRLSHRLSLCTGWYSSNTRFTITLNYKDLTGDE	60
Qy	61	ETLASYGVSGDLICILIQDDIPAPNIPSTDSHSLQNEQPSLATSSNQTSMQDEQP	120
Db	61	ETLASYGVSGDLICILIQDDIPAPNIPSTDSHSLQNEQPSLATSSNQTSMQDEQP	120
Qy	121	SDSFQGAAGQGVNDDMLGPGNFAESIQDNNAHMAEGTGFYPSBPMLCSBSVEGOVP	180
Db	121	SDSFQGAAGQGVNDDMLGPGNFAESIQDNNAHMAEGTGFYPSBPMLCSBSVEGOVP	180
Qy	181	HSLETLQSQADCDANDALIVLHLLMLESYIPQGTQTEAKALSMPEKWLKSGVYKQYMH	240
Db	181	HSLETLQSQADCDANDALIVLHLLMLESYIPQGTQTEAKALSMPEKWLKSGVYKQYMH	240
Qy	241	PLCEGSSATLTCVPLGNLIVVNATLKNNEIRSVKRIQLLPESFICKEKLGENVANYKD	300
Db	241	PLCEGSSATLTCVPLGNLIVVNATLKNNEIRSVKRIQLLPESFICKEKLGENVANYKD	300

Qy 301 LQKLSRLFKDQVYVPLLAFTRAQALNLPDVFGVLVPLLELKLRIFFLLDVRSLVLSAVCR 360
Db 301 LQKLSRLFKDQVYVPLLAFTRAQALNLPDVFGVLVPLLELKLRIFFLLDVRSLVLSAVCR 360
Qy 361 DLFTASNDPLLRFLYLRDFRDNTRVQDQTDWKELYRKRHIQRKESPKGRFVMLLPSTH 420
Db 361 DLFTASNDPLLRFLYLRDFRDNTRVQDQTDWKELYRKRHIQRKESPKGRFVMLLPSTH 420
Qy 421 TIPFYNPLHPRPPSSRLPGIIGGEYDQRTPLPYVGDPISSLLPGGETPSQPPPLRP 480
Db 421 TIPFYNPLHPRPPSSRLPGIIGGEYDQRTPLPYVGDPISSLLPGGETPSQPPPLRP 480
Qy 481 RFDVPGLPGNPILPGRGGNDPRFPFRPSRGRPTDGRLSFM 522
Db 481 RFDVPGLPGNPILPGRGGNDPRFPFRPSRGRPTDGRLSFM 522
Qy 481 RFDVPGLPGNPILPGRGGNDPRFPFRPSRGRPTDGRLSFM 522
Db 481 RFDVPGLPGNPILPGRGGNDPRFPFRPSRGRPTDGRLSFM 522
RESULT 2
US-10-245-593-2
; Sequence 2, Application US/10245593
; Publication No. US20030039646A1
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: KOVALENKO, Andrei
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNG/NGF RECEPTOR H
; FILE REFERENCE: WALLACH-22A
; CURRENT APPLICATION NUMBER: US/10/245,593
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US/09/927,458
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/IL98/00125
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: IL 120485
; PRIOR FILING DATE: 1997-03-19
; PRIOR APPLICATION NUMBER: 09/381,358
; PRIOR FILING DATE: 1999-09-20
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-245-593-2
Query Match 100.0%; Score 2754; DB 4; Length 522;
Best Local Similarity 100.0%; Pred. No. 2.6e-223;
Matches 522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRLRVLLKRTWPLEVPETEPTLGHLSRLSLCTWGYSSNTRFTITLNYKDLPTGDE 60
Db 1 MRLRVLLKRTWPLEVPETEPTLGHLSRLSLCTWGYSSNTRFTITLNYKDLPTGDE 60
Qy 61 ETLASYGIVSGDLICLIQDDIPAPNIPSSDSEHSSLONNQPSLATSSNQTSMQDEQP 120
Db 61 ETLASYGIVSGDLICLIQDDIPAPNIPSSDSEHSSLONNQPSLATSSNQTSMQDEQP 120
Qy 121 SDSFGQAAQSGVWDDSMGLGSPNFQFEAESIQDNAHMAEGTGFYSEPMLCSESVEGQVP 180
Db 121 SDSFGQAAQSGVWDDSMGLGSPNFQFEAESIQDNAHMAEGTGFYSEPMLCSESVEGQVP 180
Qy 181 HSLETLQSDACSDANDALIIVLIHLLMESGYIQGTEAKALSMPEKWLKSGVYKLYMH 240
Db 181 HSLETLQSDACSDANDALIIVLIHLLMESGYIQGTEAKALSMPEKWLKSGVYKLYMH 240
Qy 241 PLCEGSSATLTCVPLGNLIIVNATLKINNEIRSVKRLQLLPESFICKEKLGENVANIYKD 300
Db 241 PLCEGSSATLTCVPLGNLIIVNATLKINNEIRSVKRLQLLPESFICKEKLGENVANIYKD 300
Qy 301 LQKLSRLFKDQVYVPLLAFTRAQALNLPDVFGVLVPLLELKLRIFFLLDVRSLVLSAVCR 360
Db 301 LQKLSRLFKDQVYVPLLAFTRAQALNLPDVFGVLVPLLELKLRIFFLLDVRSLVLSAVCR 360
Qy 361 DLFTASNDPLLRFLYLRDFRDNTRVQDQTDWKELYRKRHIQRKESPKGRFVMLLPSTH 420
Db 361 DLFTASNDPLLRFLYLRDFRDNTRVQDQTDWKELYRKRHIQRKESPKGRFVMLLPSTH 420
Qy 421 TIPFYNPLHPRPPSSRLPGIIGGEYDQRTPLPYVGDPISSLLPGGETPSQPPPLRP 480
Db 421 TIPFYNPLHPRPPSSRLPGIIGGEYDQRTPLPYVGDPISSLLPGGETPSQPPPLRP 480
Qy 481 RFDVPGLPGNPILPGRGGNDPRFPFRPSRGRPTDGRLSFM 522
Db 481 RFDVPGLPGNPILPGRGGNDPRFPFRPSRGRPTDGRLSFM 522

Qy 361 DLFTASNDPLLRFLYLRDFRDNTRVQDQTDWKELYRKRHIQRKESPKGRFVMLLPSTH 420
Db 361 DLFTASNDPLLRFLYLRDFRDNTRVQDQTDWKELYRKRHIQRKESPKGRFVMLLPSTH 420
Qy 421 TIPFYNPLHPRPPSSRLPGIIGGEYDQRTPLPYVGDPISSLLPGGETPSQPPPLRP 480
Db 421 TIPFYNPLHPRPPSSRLPGIIGGEYDQRTPLPYVGDPISSLLPGGETPSQPPPLRP 480
Qy 481 RFDVPGLPGNPILPGRGGNDPRFPFRPSRGRPTDGRLSFM 522
Db 481 RFDVPGLPGNPILPGRGGNDPRFPFRPSRGRPTDGRLSFM 522
RESULT 3
US-10-679-246-10
; Sequence 10, Application US/10679246
; Publication No. US20040163138A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Matsuzawa, Shu-ichi
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; FILE REFERENCE: in Protein Degradation, Products and Methods Related Thereto
; FILE REFERENCE: 66821-235
; CURRENT APPLICATION NUMBER: US/10/679,246
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 09/591,694
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-679-246-10
Query Match 99.6%; Score 2744; DB 4; Length 522;
Best Local Similarity 99.6%; Pred. No. 1.8e-222;
Matches 520; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MRLRVLLKRTWPLEVPETEPTLGHLSRLSLCTWGYSSNTRFTITLNYKDLPTGDE 60
Db 1 MRLRVLLKRTWPLEVPETEPTLGHLSRLSLCTWGYSSNTRFTITLNYKDLPTGDE 60
Qy 61 ETLASYGIVSGDLICLIQDDIPAPNIPSSDSEHSSLONNQPSLATSSNQTSMQDEQP 120
Db 61 ETLASYGIVSGDLICLIQDDIPAPNIPSSDSEHSSLONNQPSLATSSNQTSMQDEQP 120
Qy 121 SDSFGQAAQSGVWDDSMGLGSPNFQFEAESIQDNAHMAEGTGFYSEPMLCSESVEGQVP 180
Db 121 SDSFGQAAQSGVWDDSMGLGSPNFQFEAESIQDNAHMAEGTGFYSEPMLCSESVEGQVP 180
Qy 181 HSLETLQSDACSDANDALIIVLIHLLMESGYIQGTEAKALSMPEKWLKSGVYKLYMH 240
Db 181 HSLETLQSDACSDANDALIIVLIHLLMESGYIQGTEAKALSMPEKWLKSGVYKLYMH 240
Qy 241 PLCEGSSATLTCVPLGNLIIVNATLKINNEIRSVKRLQLLPESFICKEKLGENVANIYKD 300
Db 241 PLCEGSSATLTCVPLGNLIIVNATLKINNEIRSVKRLQLLPESFICKEKLGENVANIYKD 300
Qy 301 LQKLSRLFKDQVYVPLLAFTRAQALNLPDVFGVLVPLLELKLRIFFLLDVRSLVLSAVCR 360
Db 301 LQKLSRLFKDQVYVPLLAFTRAQALNLPDVFGVLVPLLELKLRIFFLLDVRSLVLSAVCR 360
Qy 361 DLFTASNDPLLRFLYLRDFRDNTRVQDQTDWKELYRKRHIQRKESPKGRFVMLLPSTH 420
Db 361 DLFTASNDPLLRFLYLRDFRDNTRVQDQTDWKELYRKRHIQRKESPKGRFVMLLPSTH 420
Qy 421 TIPFYNPLHPRPPSSRLPGIIGGEYDQRTPLPYVGDPISSLLPGGETPSQPPPLRP 480
Db 421 TIPFYNPLHPRPPSSRLPGIIGGEYDQRTPLPYVGDPISSLLPGGETPSQPPPLRP 480
Qy 481 RFDVPGLPGNPILPGRGGNDPRFPFRPSRGRPTDGRLSFM 522
Db 481 RFDVPGLPGNPILPGRGGNDPRFPFRPSRGRPTDGRLSFM 522

; PRIOR APPLICATION NUMBER: 60/078,577
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,563
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,313
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 200
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (115)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-397-945-200

Query Match 87.3%; Score 2404; DB 3; Length 462;
Best Local Similarity 88.1%; Pred. No. 7.6e-194;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

Qy 1 MRLVRLLKRTWPLEVPEPETETGLHLSHLRLSLCTGWYSSNTRFTITLNYKDPPLTGDE 60
Db 1 MRLVRLLKRTWPLEVPEPETETGLHLSHLRLSLCTGWYSSNTRFTITLNYKDPPLTGDE 60

Qy 61 ETLASYGIVSGDLICLLIQDDIPAPNIPSSDSEHSLQNNQPSLATSSNOTSMQDEQP 120
Db 61 ETLASYGIVSGDLICLLIQDDIPAPNIPSSDSEHSLQNNQPSLATSSNOTSMQDEQP 120

Qy 121 SDSFQGAQAGVWDDSMGLPSONFEAESIQDHAHMAEGTGYFSPMLCSSEVEGQVP 180
Db 121 SDSFQGAQAGVWDDSMGLPSONFEAESIQDHAHMAEGTGYFSPMLCSSEVEGQVP 180

Qy 181 HSLETLQSDADCSANDALIVLHLLMESGYIQGTEAKALSMPKWKLSGVYKQYMH 240
Db 181 HSLETLQSDADCSANDALIVLHLLMESGYIQGTEAKALSMPKWKLSGVYKQYMH 240

Qy 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPESFICKELGENVANIYKD 300
Db 241 PLCEGSSATLTCVPLGNLIVN----- 262

Qy 301 LQKLSRLFKQDLVYPLLAFTQALNLPDVFLVPLLELKLIRIFRLLDVRSVLSAVCR 360
Db 263 -----ALNLPDVFLVPLLELKLIRIFRLLDVRSVLSAVCR 300

Qy 361 DLFTASNDPILLWRFLYLRDRDNTVRVQDQDWKELYRKRHIQRKESPKGRFVMLLPSSSTH 420
Db 301 DLFTASNDPILLWRFLYLRDRDNTVRVQDQDWKELYRKRHIQRKESPKGRFVMLLPSSSTH 360

Qy 421 TIFYPNPLHPRPPSSRLPGIIGGYDQRPPLPYVGDPISSLIPOGGETPSQFPPLRP 480
Db 361 TIFYPNPLHPRPPSSRLPGIIGGYDQRPPLPYVGDPISSLIPOGGETPSQFPPLRP 420

Qy 481 RFDVGPGLPGNPILPGRGPNDRFPFRPSRGRPTDGRLSFM 522
Db 421 RFDVGPGLPGNPILPGRGPNDRFPFRPSRGRPTDGRLSFM 462

RESULT 9
US-10-264-237-2485
; Sequence 2485, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19

; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2485
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (115)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-2485

Query Match 87.3%; Score 2404; DB 4; Length 462;
Best Local Similarity 88.1%; Pred. No. 7.6e-194;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

Qy 1 MRLVRLLKRTWPLEVPEPETETGLHLSHLRLSLCTGWYSSNTRFTITLNYKDPPLTGDE 60
Db 1 MRLVRLLKRTWPLEVPEPETETGLHLSHLRLSLCTGWYSSNTRFTITLNYKDPPLTGDE 60

Qy 61 ETLASYGIVSGDLICLLIQDDIPAPNIPSSDSEHSLQNNQPSLATSSNOTSMQDEQP 120
Db 61 ETLASYGIVSGDLICLLIQDDIPAPNIPSSDSEHSLQNNQPSLATSSNOTSMQDEQP 120

Qy 121 SDSFQGAQAGVWDDSMGLPSONFEAESIQDHAHMAEGTGYFSPMLCSSEVEGQVP 180
Db 121 SDSFQGAQAGVWDDSMGLPSONFEAESIQDHAHMAEGTGYFSPMLCSSEVEGQVP 180

Qy 181 HSLETLQSDADCSANDALIVLHLLMESGYIQGTEAKALSMPKWKLSGVYKQYMH 240
Db 181 HSLETLQSDADCSANDALIVLHLLMESGYIQGTEAKALSMPKWKLSGVYKQYMH 240

Qy 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPESFICKELGENVANIYKD 300
Db 241 PLCEGSSATLTCVPLGNLIVN----- 262

Qy 301 LQKLSRLFKQDLVYPLLAFTQALNLPDVFLVPLLELKLIRIFRLLDVRSVLSAVCR 360
Db 263 -----ALNLPDVFLVPLLELKLIRIFRLLDVRSVLSAVCR 300

Qy 361 DLFTASNDPILLWRFLYLRDRDNTVRVQDQDWKELYRKRHIQRKESPKGRFVMLLPSSSTH 420
Db 301 DLFTASNDPILLWRFLYLRDRDNTVRVQDQDWKELYRKRHIQRKESPKGRFVMLLPSSSTH 360

Qy 421 TIFYPNPLHPRPPSSRLPGIIGGYDQRPPLPYVGDPISSLIPOGGETPSQFPPLRP 480
Db 361 TIFYPNPLHPRPPSSRLPGIIGGYDQRPPLPYVGDPISSLIPOGGETPSQFPPLRP 420

Qy 481 RFDVGPGLPGNPILPGRGPNDRFPFRPSRGRPTDGRLSFM 522
Db 421 RFDVGPGLPGNPILPGRGPNDRFPFRPSRGRPTDGRLSFM 462

RESULT 10
US-10-653-595-200
; Sequence 200, Application US/10653595
; Publication No. US20040048304A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et. al.
; TITLE OF INVENTION: 95 Human secreted proteins
; FILE REFERENCE: P2027P1C1
; CURRENT APPLICATION NUMBER: US/10/653,595
; CURRENT FILING DATE: 2003-09-03
; PRIOR APPLICATION NUMBER: US 09/397945
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/05804
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,566
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,576
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,573
; PRIOR FILING DATE: 1998-03-19

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; PRIOR APPLICATION NUMBER: 60/078,574
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,579
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,314
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080,312
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/078,578
; PRIOR FILING DATE: 1998-03-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 200
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (115)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-653-595-200

Query Match      87.3%; Score 2404; DB 4; Length 462;
Best Local Similarity 88.1%; Pred. No. 7,6e-194;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

QY 1 MRLVRLKRWLPLEVPETETLGHLSRLSLCTWGYSSNTFTITLNYKDLPTGDE 60
DB 1 MRLVRLKRWLPLEVPETETLGHLSRLSLCTWGYSSNTFTITLNYKDLPTGDE 60

QY 61 ETLASYGVSGDLICLIQDDIPAPNIPSSSTDSEHSSLQNNNEQPSLATSSNOTSMQDSQP 120
DB 61 ETLASYGVSGDLICLIQDDIPAPNIPSSSTDSEHSSLQNNNEQPSLATSSNOTSMQDSQP 120

QY 121 SDSFGQAAQSGVWDDSMGLPSONFEAESIQDNAHMAEGTGFPSEPMLCSESVEGQVP 180
DB 121 SDSFGQAAQSGVWDDSMGLPSONFEAESIQDNAHMAEGTGFPSEPMLCSESVEGQVP 180

QY 181 HSLETLYOSADCSANDALIVLIHLLMESGYIQGTAKALSMPEKWLKSGVYKLYMH 240
DB 181 HSLETLYOSADCSANDALIVLIHLLMESGYIQGTAKALSMPEKWLKSGVYKLYMH 240

QY 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPSPFCICEKLGENVANIYKD 300
DB 241 PLCEGSSATLTCVPLGNLIVVN-----ALNLPDVFGVLVPLLELKLRI 262

QY 301 LQKLSRLFKDQLVYPLLAFTQALNLPDVFGVLVPLLELKLRI 360
DB 263 -----ALNLPDVFGVLVPLLELKLRI 300

QY 361 DLFTASNDPLLRFLYLRDPRNTVRVQDTPWKELRYKRHIQKESPKGRFVMLLPSSSTH 420
DB 301 DLFTASNDPLLRFLYLRDPRNTVRVQDTPWKELRYKRHIQKESPKGRFVMLLPSSSTH 360

QY 421 TIPFPNPLHPRPFSSRLPGIIGGEYDQRTPLPVGDPISLLIPGGETPSQPPPLRP 480
DB 361 TIPFPNPLHPRPFSSRLPGIIGGEYDQRTPLPVGDPISLLIPGGETPSQPPPLRP 420

QY 481 RFPDPVGLPGNPILPGRGPNDRFPFRPSRGRPTDGRLSFM 522
DB 421 RFPDPVGLPGNPILPGRGPNDRFPFRPSRGRPTDGRLSFM 462

RESULT 11
US-09-397-945-435
; Sequence 435, Application US/09397945
; Publication No. US20030065139A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: 95 Human secreted proteins
; FILE REFERENCE: P2027P1
; CURRENT APPLICATION NUMBER: US/09/397,945
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; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/05804
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,566
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,576
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,573
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,574
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,579
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,314
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080,312
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/078,578
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,581
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,577
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,563
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,313
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 435
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (150)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-397-945-435

Query Match      87.3%; Score 2404; DB 3; Length 497;
Best Local Similarity 88.1%; Pred. No. 8,5e-194;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

QY 1 MRLVRLKRWLPLEVPETETLGHLSRLSLCTWGYSSNTFTITLNYKDLPTGDE 60
DB 36 MRLVRLKRWLPLEVPETETLGHLSRLSLCTWGYSSNTFTITLNYKDLPTGDE 95

QY 61 ETLASYGVSGDLICLIQDDIPAPNIPSSSTDSEHSSLQNNNEQPSLATSSNOTSMQDSQP 120
DB 96 ETLASYGVSGDLICLIQDDIPAPNIPSSSTDSEHSSLQNNNEQPSLATSSNOTSMQDSQP 155

QY 121 SDSFGQAAQSGVWDDSMGLPSONFEAESIQDNAHMAEGTGFPSEPMLCSESVEGQVP 180
DB 156 SDSFGQAAQSGVWDDSMGLPSONFEAESIQDNAHMAEGTGFPSEPMLCSESVEGQVP 215

QY 181 HSLETLYOSADCSANDALIVLIHLLMESGYIQGTAKALSMPEKWLKSGVYKLYMH 240
DB 216 HSLETLYOSADCSANDALIVLIHLLMESGYIQGTAKALSMPEKWLKSGVYKLYMH 275

QY 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPSPFCICEKLGENVANIYKD 300
DB 276 PLCEGSSATLTCVPLGNLIVVN-----ALNLPDVFGVLVPLLELKLRI 297

QY 301 LQKLSRLFKDQLVYPLLAFTQALNLPDVFGVLVPLLELKLRI 360
DB 298 -----ALNLPDVFGVLVPLLELKLRI 335

QY 361 DLFTASNDPLLRFLYLRDPRNTVRVQDTPWKELRYKRHIQKESPKGRFVMLLPSSSTH 420
DB 336 DLFTASNDPLLRFLYLRDPRNTVRVQDTPWKELRYKRHIQKESPKGRFVMLLPSSSTH 395

QY 421 TIPFPNPLHPRPFSSRLPGIIGGEYDQRTPLPVGDPISLLIPGGETPSQPPPLRP 480
DB 421 TIPFPNPLHPRPFSSRLPGIIGGEYDQRTPLPVGDPISLLIPGGETPSQPPPLRP 480
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Db 396 TIFYPNPLHPRPPSSRLPGIIGGEYDQRPTLPYVGDPISLIPGGETPSQFPPLRP 455
Qy 481 RFDVGPGLPGNPILPGRGGNDPFRPPSRGRPTDGRLSFM 522
Db 456 RFDVGPGLPGNPILPGRGGNDPFRPPSRGRPTDGRLSFM 497

RESULT 12

US-10-653-595-435
; Sequence 435, Application US/10653595
; Publication No. US20040048304A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et. al.
; TITLE OF INVENTION: 95 Human secreted proteins
; FILE REFERENCE: P2027P1C1
; CURRENT APPLICATION NUMBER: US/10/653,595
; CURRENT FILING DATE: 2003-09-03
; PRIOR APPLICATION NUMBER: US 09/397945
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/05804
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,566
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,576
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,573
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,574
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,579
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,314
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080,312
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/078,578
; PRIOR FILING DATE: 1998-03-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 435
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (150)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-653-595-435

Query Match 87.3%; Score 2404; DB 4; Length 497;
Best Local Similarity 88.1%; Pred. No. 8.5e-194;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;
Qy 1 MRLRVLLKRTWPLEVETETPTLGLHLSHLRLSLCTGWYSSNTRFTITILNYKDPLTGD 60
Db 36 MRLRVLLKRTWPLEVETETPTLGLHLSHLRLSLCTGWYSSNTRFTITILNYKDPLTGD 95
Qy 61 ETLASYGIVSGDLICLLIQLDDIPAPNIPSSSTDSEHSLQNEQPSLATSSNOTSQDEQP 120
Db 96 ETLASYGIVSGDLICLLIQLDDIPAPNIPSSSTDSEHSLQNEQPSLATSSNOTSQDEQP 155
Qy 121 SDSFQQAAGSGVWDDSMGLPSONFEASIQDNAHMAEGTGYFPPSPMLCSSESVEGQVP 180
Db 156 SDSFQQAAGSGVWDDSMGLPSONFEASIQDNAHMAEGTGYFPPSPMLCSSESVEGQVP 215
Qy 181 HSLETLQYQADCSANDALIVLHLLMLESYGYPQGTAKALSMPEKWKLSGVYKLYQM 240
Db 216 HSLETLQYQADCSANDALIVLHLLMLESYGYPQGTAKALSMPEKWKLSGVYKLYQM 275
Qy 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPESFICKEKLGENVANIYKD 300
Db 276 PLCEGSSATLTCVPLGNLIVN----- 297

Qy 301 LQKLSRLFKDQLVYPLLAFTQALNLPDVFGLVVLPLELKLIRIFRLLDVRSVLSAVCR 360
Db 298 -----ALNLPDVFGLVVLPLELKLIRIFRLLDVRSVLSAVCR 335
Qy 361 DLFTASNDPPLLWRFLYLRDFRDNTRVQDQTDWKELYKRKHIOKESPKGRFVMLLPSTH 420
Db 336 DLFTASNDPPLLWRFLYLRDFRDNTRVQDQTDWKELYKRKHIOKESPKGRFVMLLPSTH 395
Qy 421 TIFYPNPLHPRPPSSRLPGIIGGEYDQRPTLPYVGDPISLIPGGETPSQFPPLRP 480
Db 396 TIFYPNPLHPRPPSSRLPGIIGGEYDQRPTLPYVGDPISLIPGGETPSQFPPLRP 455
Qy 481 RFDVGPGLPGNPILPGRGGNDPFRPPSRGRPTDGRLSFM 522
Db 456 RFDVGPGLPGNPILPGRGGNDPFRPPSRGRPTDGRLSFM 497
RESULT 13
US-10-679-246-8
; Sequence 8, Application US/10679246
; Publication No. US20040163138A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Matsuzawa, Shu-ichi
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; FILE REFERENCE: 66821-235
; CURRENT APPLICATION NUMBER: US/10/679,246
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 09/591,694
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-679-246-8
Query Match 82.4%; Score 2270; DB 4; Length 443;
Best Local Similarity 99.8%; Pred. No. 1.5e-182;
Matches 430; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 92 DSEHSSLQNEQPSLATSSNOTSQDEQPSDSFQQAAGSGVWDDSMGLPSONFEAS 151
Db 13 DSEHSSLQNEQPSLATSSNOTSQDEQPSDSFQQAAGSGVWDDSMGLPSONFEAS 72
Qy 152 QDNAHMAEGTGYFPPSPMLCSSESVEGQVPHSLFTLYQSADCSANDALIVLHLLMLES 211
Db 73 QDNAHMAEGTGYFPPSPMLCSSESVEGQVPHSLFTLYQSADCSANDALIVLHLLMLES 132
Qy 212 YIPQGTAKALSMPEKWKLSGVYKLYQMHPCLCGSSATLTCVPLGNLIVNATLKINNEI 271
Db 133 YIPQGTAKALSMPEKWKLSGVYKLYQMHPCLCGSSATLTCVPLGNLIVNATLKINNEI 192
Qy 272 RSVKRLQLLPESFICKEKLGENVANIYKDQLKLSRLFKDQLVYPLLAFTQALNLPDVF 331
Db 193 RSVKRLQLLPESFICKEKLGENVANIYKDQLKLSRLFKDQLVYPLLAFTQALNLPDVF 252
Qy 332 LVVLPLELKLIRIFRLLDVRSVLSAVCRDLFTASNDPPLLWRFLYLRDFRDNTRVQD 391
Db 253 LVVLPLELKLIRIFRLLDVRSVLSAVCRDLFTASNDPPLLWRFLYLRDFRDNTRVQD 312
Qy 392 WKELYKRKHIOKESPKGRFVMLLPSTHTIPIYPNPLHPRPPSSRLPGIIGGEYDQR 451
Db 313 WKELYKRKHIOKESPKGRFVMLLPSTHTIPIYPNPLHPRPPSSRLPGIIGGEYDQR 372
Qy 452 PTLPYVGDPISLIPGGETPSQFPPLRPDPVGPPLPGNPILPGRGGNDPFRPPSR 511
Db 373 PTLPYVGDPISLIPGGETPSQFPPLRPDPVGPPLPGNPILPGRGGNDPFRPPSR 432
Qy 512 GRPTDGRLSFM 522

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Db 433 GRPTDGRLSFM 443
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RESULT 14
US-10-450-763-48869
; Sequence 48869, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790C1P3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 48869
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(549)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-48869

Query Match 75.8%; Score 2086.5; DB 5; Length 549;
Best Local Similarity 80.8%; Pred. No. 6.2e-167;
Matches 438; Conservative 15; Mismatches 64; Indels 25; Gaps 18;

Qy 3 LRVLKKTWPLEVET--EPTLGHRLGHLRLSLCTWGYSSNTFTITLNYKDLPTGDE 60
Db 2 LRVLKKTWPLEVETGARTGGILRSHLRSLCTWGYSSNTFTITLNYKDLPTGDE 61

Qy 61 ETLASYGIVSGDLICLLIQDDIPAPNIPSSSTDSEHSSIQNNBQPSLATSSNQTSMDQEP 120
Db 62 ETLASYGIVSGDLICLLIQDDIPAPNIPSSSTDSEHSSIQNNBQPSLATSSNQTSMDQEP 121

Qy 121 SDSFGQAAQSGVWDDSMGLGPSQNFESIQDQNAHMAEGTGFYSEPMKLS 177
Db 122 SDSFGQAAQSGVWDDSMGLGPSQNFESIQDQNAHMAEGTGFYSEPMKLS 180

Qy 178 QVPHSLETLYQSADCSANDALIIVLIHLLMLESYIPQGTAKALSMPEKWKLSGVYKIQ 237
Db 191 QVPHSLETLYQLAUCSDANDALIIVLIHLLMLESYIPQGTAKALSMPEKWKLSGVYKIQ 240

Qy 238 YMHPLCEGSSATLTCVPLGNLIVVNATLKINNEIRS-VKRLQLLPESFICKEKLGENVAN 296
Db 241 YMHPLCEGSSVTLTCVPLGNLIVVNATLKINNEIRKCKKGCSSLPSFICKEKLGENVAN 300

Qy 297 IYKDLQKLSRLFKDQLVYPLLAFTQALNLPDVFGLVPLPLELKLRIFRLLDVRSL 356
Db 301 IYKDLQKLSRLFKDQLAHPLLAFTQALNLPDVFGLVPLPLELKLRIFRLLDVRSL 360

Qy 357 AVCRLDFTASNDPLLRFLYL-RDRFNTVRVQDQTDWKELY--RKRHIQRKESPKGR--F 411
Db 361 AVCRLDFTASNDPLLRVYFICVNFDRNTVRVQDQTDWERTVQGRRAHTKEKESPKGRVLW 420

Qy 412 VMLPSSSTHTIPFPNPL-HPR-PPFS--SRLLPPIIGGEY--DQRPTLPYVGDPISSLI 466
Db 421 MLLAIRQTHTIPFPYQPLWHPRGHFKLPAPPPGIYSGWNNMDQRTFPYVGRTOSSSLN 480

Qy 467 G--PGETPS-QFPPLRPDPVGP-LPGPN-PILP-GRGGPNDRF-PFRPSRGR-PTDGR 518
Db 481 SWLGETPKPSFLPLRPDPVWHPFGPPSPSLPRARAGPNDQISPPRPOQSGQLIGR 540

Qy 519 LS 520
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Db 541 LS 542
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RESULT 15
US-10-264-237-2484
; Sequence 2484, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2484
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-264-237-2484

Query Match 55.4%; Score 1527; DB 4; Length 317;
Best Local Similarity 94.0%; Pred. No. 4.6e-120;
Matches 300; Conservative 4; Mismatches 11; Indels 4; Gaps 2;

Qy 115 MQDEQPSDSFOGQAAQSGVWDDSMGLGPSQNFESIQDQNAHMAEGTGFYSEPMKLS 174
Db 1 MQDEQPSDSFOGQAAQSGVWDDSMGLGPSQNFESIQDQNAHMAEGTGFYSEPMKLS 60

Qy 175 VEGQVPHSLETLYQSADCSANDALIIVLIHLLMLESYIPQGTAKALSMPEKWKLSGVY 234
Db 61 VEGQVPHSLETLYQSADCSANDALIIVLIHLLMLESYIPQGTAKALSMPEKWKLSGVY 120

Qy 235 KLOYMHPICEGSSATLTCVPLGNLIVVNATLKINNEIRS-VKRLQLLPESFICKEKLGENV 294
Db 121 KLOYMHPICEGSSATLTCVPLGNLIVVNATLKINNEIRS-VKRLQLLPESFICKEKLGENV 180

Qy 295 ANIYKDLQKLSRLFKDQLVYPLLAFTQALNLPDVFGLVPLPLELKLRIFRLLDVRSL 354
Db 181 ANIYKDLQKLSRLFKDQLVYPLLAFTQALNLPDVFGLVPLPLELKLRIFRLLDVRSL 240

Qy 355 LSACVCRDLFTASNDPLLRFLYL-RDRFNTVRVQDQTDWKELYRKRHIQRKESPKGRF--V 412
Db 241 LSACVCRDLFTASNDPLLRFLYL-RDRFNTVRVQDQTDWKELYRKRHIQRKESPKGRVCA 300

Qy 413 MLLPSSSTHTIPFPNPLHP 431
Db 301 PAIVNSHHSI--LSOPLAP 317

Search completed: February 14, 2006, 21:16:27
Job time : 171 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 14, 2006, 21:13:48 ; Search time 17 Seconds
(without alignments)
402.939 Million cell updates/sec

Title: US-09-927-458-2
Perfect score: 2754
Sequence: 1 MRLVRLLKRWPLEVPETE.....DRPFPRSGRPTDGRLSFM 522

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2489	90.4	482	6	US-10-632-150-14 Sequence 14, Appl
2	2489	90.4	482	7	US-11-073-457-14 Sequence 14, Appl
3	2489	90.4	482	7	US-11-073-460-14 Sequence 14, Appl
4	194	7.0	39	6	US-10-632-150-21 Sequence 21, Appl
5	194	7.0	39	7	US-11-073-457-21 Sequence 21, Appl
6	194	7.0	39	7	US-11-073-460-21 Sequence 21, Appl
7	139	5.0	327	6	US-10-632-150-58 Sequence 58, Appl
8	139	5.0	327	7	US-11-073-457-58 Sequence 58, Appl
9	139	5.0	327	7	US-11-073-460-58 Sequence 58, Appl
10	114.5	4.2	346	7	US-11-036-256-33 Sequence 33, Appl
11	114	4.1	2432	6	US-10-821-234-899 Sequence 899, App
12	109.5	4.0	791	6	US-10-821-234-962 Sequence 962, App
13	106.5	3.9	200	7	US-11-036-256-27 Sequence 27, Appl
14	106.5	3.9	228	7	US-11-036-256-31 Sequence 31, Appl
15	105	3.8	398	7	US-11-150-845-10 Sequence 10, Appl
16	105	3.8	398	7	US-11-150-847-10 Sequence 10, Appl
17	105	3.8	502	7	US-11-122-795-14 Sequence 14, Appl
18	105	3.8	502	7	US-11-150-845-2 Sequence 2, Appli
19	105	3.8	502	7	US-11-149-945-1 Sequence 1, Appli
20	105	3.8	502	7	US-11-150-487-2 Sequence 2, Appli
21	105	3.8	609	7	US-11-150-845-20 Sequence 20, Appl
22	105	3.8	609	7	US-11-150-487-20 Sequence 20, Appl
23	105	3.8	649	7	US-11-150-845-18 Sequence 18, Appl
24	105	3.8	649	7	US-11-150-845-22 Sequence 22, Appl
25	105	3.8	649	7	US-11-150-487-18 Sequence 18, Appl

26	105	3.8	649	7	US-11-150-487-22	Sequence 22, Appl
27	105	3.8	715	7	US-11-150-845-14	Sequence 14, Appl
28	105	3.8	715	7	US-11-150-487-14	Sequence 14, Appl
29	102.5	3.7	116	7	US-11-036-256-25	Sequence 25, Appl
30	101.5	3.7	411	7	US-11-036-256-89	Sequence 89, Appl
31	100.5	3.6	860	7	US-11-172-410-2	Sequence 2, Appli
32	100.5	3.6	915	6	US-10-821-234-1514	Sequence 1514, Ap
33	99.5	3.6	175	6	US-10-821-234-1074	Sequence 1074, Ap
34	99	3.6	552	6	US-10-821-234-1022	Sequence 1022, Ap
35	98.5	3.6	1187	6	US-10-821-234-955	Sequence 955, App
36	98	3.6	1076	6	US-10-467-557-7916	Sequence 7916, Ap
37	97.5	3.5	183	7	US-11-036-256-21	Sequence 21, Appl
38	97.5	3.5	16990	7	US-11-175-689-7	Sequence 7, Appli
39	97	3.5	1377	6	US-10-821-234-1070	Sequence 1002, Ap
40	95.5	3.5	628	6	US-10-995-561-1003	Sequence 1003, Ap
41	95.5	3.5	915	6	US-10-995-561-1000	Sequence 1000, Ap
42	95.5	3.5	917	6	US-10-995-561-1000	Sequence 1004, Ap
43	95.5	3.5	940	6	US-10-995-561-1004	Sequence 2, Appli
44	95.5	3.5	963	6	US-10-467-962B-2	Sequence 1001, Ap
45	95.5	3.5	969	6	US-10-995-561-1001	

ALIGNMENTS

RESULT 1
US-10-632-150-14
; Sequence 14, Application US/10632150
; Publication No. US20050251871A1
; GENERAL INFORMATION:
; APPLICANT: Chaur, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/632.150
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-632-150-14

Query Match 90.4%; Score 2489; DB 6; Length 482;
Best Local Similarity 98.1%; Pred. No. 2.1e-200;
Matches 472; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy	42	SNTRFTITLNYKDPITGDEETLASYGIVSGDLICLILODDIPAPNIPSSSTDSEHSSLONN	101
Db	2	SNTRFTITLNYKDPITGDEETLASYGIVSGDLICLILODDIPAPNIPSSSTDSEHSSLONN	61
Qy	102	EQPSLATSSNOTSMQDEQPSDSFQQAQSGVWVNDMSMLGSPQNFAESIQDNNAHMAEGT	161
Db	62	EQPSLATSSNOTSIQDEQPSDSFQQAQSGVWVNDMSMLGSPQNFAESIQDNNAHMAEGT	121
Qy	162	GFYPSPEMLCSSEVGVQPHSLTETLQSDACSDANDALIVLIHLLMESGYIPQGTAKA	221
Db	122	GFYPSPEMLCSSEVGVQPHSLTETLQSDACSDANDALIVLIHLLMESGYIPQGTAKA	181
Qy	222	LSMPEKWLKSGVYKLYQWHPHLCGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLP	281
Db	182	LSPKWLKSGVYKLYQWHPHLCGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLP	241

Qy 282 ESFICKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTQALNLPDVFGVLVPLELKL 341
Db 242 ESFICKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTQALNLPVFGVLVPLELKL 301
Qy 342 RIFRLLDVRSVLSLSAVCRDLFTASNDPPLLWRFLYLDRFRDNTVRVQDQDWKELYRKHHI 401
Db 302 RIFRLLDVRSVLSLSAVCRDLFTASNDPPLLWRFLYLDRFRDNTVRVQDQDWKELYRKHHI 361
Qy 402 QRKESPKGRFVMLLPSSSTHTTIPFPNPLHPRFPSSRLPPGIIIGEYDQRTPLPVVGDPPI 461
Db 362 QRKESPKGRFVLLLPSSSTHTTIPFPNPLHPRFPSSRLPPGIIIGEYDQRTPLPVVGDPPI 421
Qy 462 SSLIPGGETSPQPPPLRPDPVGPPLPGPNPILPGRGPNDRPFPRSRGRPTDGRLSF 521
Db 422 SSLIPGGETSPQPPPLRPDPVGPPLPGPNPILPGRGPNDRPFPRSRGRPTDGRLSF 481
Qy 522 M 522
Db 482 M 482
RESULT 2
US-11-073-457-14
; Sequence 14, Application US/11073457
; Publication No. US20050260556A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIF
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,457
; PRIOR FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-457-14
Query Match 90.4%; Score 2489; DB 7; Length 482;
Best Local Similarity 98.1%; Pred. No. 2.1e-200;
Matches 472; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
Qy 42 SNTRFTITLNYKDPDTGDEETLASYGIVSGDLICLILODDIPAPNIPSTDSHSSLQNN 101
Db 2 SNTRFTITLNYKDPDTGDEETLASYGIVSGDLICLILODDIPAPNIPSTDSHSSLQNN 61
Qy 102 EQPSLATSSNOTSMODEQPSDFQQAQSGVWDDSMLGPSQNFPEAESIQDNAHMAEGT 161
Db 62 EQPSLATSSNOTSIQDEQPSDFQQAQSGVWDDSMLGPSQNFPEAESIQDNAHMAEGT 121
Qy 162 GFYSEPMCLSESVEGQVPHSLETLYQSADCSNDALIVLIHLLMLESYGVIPOQTEAKA 221
Db 122 GFYSEPMCLSESVEGQVPHSLETLYQSADCSNDALIVLIHLLMLESYGVIPOQTEAKA 181
Qy 222 LSMPKWKLSGVYKLYQWHPCLCEGSSATLTCTVPLGNLIVVATLKINNEIRSVKRLQLLP 281
Db 182 LSLPEKWKLSGVYKLYQWHPCLCEGSSATLTCTVPLGNLIVVATLKINNEIRSVKRLQLLP 241
Qy 282 ESFICKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTQALNLPDVFGVLVPLELKL 341
Db 242 ESFICKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTQALNLPVFGVLVPLELKL 301
Qy 342 RIFRLLDVRSVLSLSAVCRDLFTASNDPPLLWRFLYLDRFRDNTVRVQDQDWKELYRKHHI 401
Db 302 RIFRLLDVRSVLSLSAVCRDLFTASNDPPLLWRFLYLDRFRDNTVRVQDQDWKELYRKHHI 361
Qy 402 QRKESPKGRFVMLLPSSSTHTTIPFPNPLHPRFPSSRLPPGIIIGEYDQRTPLPVVGDPPI 461
Db 362 QRKESPKGRFVLLLPSSSTHTTIPFPNPLHPRFPSSRLPPGIIIGEYDQRTPLPVVGDPPI 421
Qy 462 SSLIPGGETSPQPPPLRPDPVGPPLPGPNPILPGRGPNDRPFPRSRGRPTDGRLSF 521
Db 422 SSLIPGGETSPQPPPLRPDPVGPPLPGPNPILPGRGPNDRPFPRSRGRPTDGRLSF 481
Qy 522 M 522
Db 482 M 482

Db 362 QRKESPKGRFVLLLPSSSTHTTIPFPNPLHPRFPSSRLPPGIIIGEYDQRTPLPVVGDPPI 421
Qy 462 SSLIPGGETSPQPPPLRPDPVGPPLPGPNPILPGRGPNDRPFPRSRGRPTDGRLSF 521
Db 422 SSLIPGGETSPQPPPLRPDPVGPPLPGPNPILPGRGPNDRPFPRSRGRPTDGRLSF 481
Qy 522 M 522
Db 482 M 482
RESULT 3
US-11-073-460-14
; Sequence 14, Application US/11073460
; Publication No. US20050272066A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIF
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,460
; PRIOR FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-460-14
Query Match 90.4%; Score 2489; DB 7; Length 482;
Best Local Similarity 98.1%; Pred. No. 2.1e-200;
Matches 472; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
Qy 42 SNTRFTITLNYKDPDTGDEETLASYGIVSGDLICLILODDIPAPNIPSTDSHSSLQNN 101
Db 2 SNTRFTITLNYKDPDTGDEETLASYGIVSGDLICLILODDIPAPNIPSTDSHSSLQNN 61
Qy 102 EQPSLATSSNOTSMODEQPSDFQQAQSGVWDDSMLGPSQNFPEAESIQDNAHMAEGT 161
Db 62 EQPSLATSSNOTSIQDEQPSDFQQAQSGVWDDSMLGPSQNFPEAESIQDNAHMAEGT 121
Qy 162 GFYSEPMCLSESVEGQVPHSLETLYQSADCSNDALIVLIHLLMLESYGVIPOQTEAKA 221
Db 122 GFYSEPMCLSESVEGQVPHSLETLYQSADCSNDALIVLIHLLMLESYGVIPOQTEAKA 181
Qy 222 LSMPKWKLSGVYKLYQWHPCLCEGSSATLTCTVPLGNLIVVATLKINNEIRSVKRLQLLP 281
Db 182 LSLPEKWKLSGVYKLYQWHPCLCEGSSATLTCTVPLGNLIVVATLKINNEIRSVKRLQLLP 241
Qy 282 ESFICKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTQALNLPDVFGVLVPLELKL 341
Db 242 ESFICKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTQALNLPVFGVLVPLELKL 301
Qy 342 RIFRLLDVRSVLSLSAVCRDLFTASNDPPLLWRFLYLDRFRDNTVRVQDQDWKELYRKHHI 401
Db 302 RIFRLLDVRSVLSLSAVCRDLFTASNDPPLLWRFLYLDRFRDNTVRVQDQDWKELYRKHHI 361
Qy 402 QRKESPKGRFVMLLPSSSTHTTIPFPNPLHPRFPSSRLPPGIIIGEYDQRTPLPVVGDPPI 461
Db 362 QRKESPKGRFVLLLPSSSTHTTIPFPNPLHPRFPSSRLPPGIIIGEYDQRTPLPVVGDPPI 421
Qy 462 SSLIPGGETSPQPPPLRPDPVGPPLPGPNPILPGRGPNDRPFPRSRGRPTDGRLSF 521
Db 422 SSLIPGGETSPQPPPLRPDPVGPPLPGPNPILPGRGPNDRPFPRSRGRPTDGRLSF 481
Qy 522 M 522

Db 482 M 482

RESULT 4

US-10-632-150-21
; Sequence 21, Application US/10632150
; Publication No. US20050251871A1
; GENERAL INFORMATION:
; APPLICANT: Chiau, D.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/632,150
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-632-150-21

Query Match 7.0%; Score 194; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 335 LPLEKLRIPLLDVRSVLSAVCRDLFTASNDPLLWR 373
Db 1 LPLEKLRIPLLDVRSVLSAVCRDLFTASNDPLLWR 39

RESULT 5

US-11-073-457-21
; Sequence 21, Application US/11073457
; Publication No. US20050260556A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,457
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-457-21

Query Match 7.0%; Score 194; DB 7; Length 39;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 335 LPLEKLRIPLLDVRSVLSAVCRDLFTASNDPLLWR 373
Db 1 LPLEKLRIPLLDVRSVLSAVCRDLFTASNDPLLWR 39

RESULT 6

US-11-073-460-21
; Sequence 21, Application US/11073460
; Publication No. US20050272066A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,460
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-460-21

Query Match 7.0%; Score 194; DB 7; Length 39;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 335 LPLEKLRIPLLDVRSVLSAVCRDLFTASNDPLLWR 373
Db 1 LPLEKLRIPLLDVRSVLSAVCRDLFTASNDPLLWR 39

RESULT 7

US-10-632-150-58
; Sequence 58, Application US/10632150
; Publication No. US20050251871A1
; GENERAL INFORMATION:
; APPLICANT: Chiau, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/632,150
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-632-150-58

Query Match 5.0%; Score 139; DB 6; Length 327;
Best Local Similarity 25.1%; Pred. No. 0.00028;
Matches 57; Conservative 32; Mismatches 64; Indels 74; Gaps 11;

Qy 291 GENVANIY----KDLQKLSRL---FKDLVYPLLAFTROALNL--PDV-----FGLVVLPL 337
Db 19 GDGVNSYIEDNDDSKMADLLSYFQQQ-----LTFQESVLKLCQPELESSQIHISVLPM 73
Qy 338 ELKLRIPL-----LDVRSVLSAVCRDLFTASNDPLLWRFLYLRDRFRONTVR-VQDTD 391
Db 74 EVLMYIFRWVSSDLDLSLEQLSVCRGYICARDPEIWRACKLVGWSGSCIKLVPTS 133
Qy 392 WKELYRKHITQRKESPKGRFVMLLPSSST-----HTIPFYPNFLHPRPF 434


```
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 899
; LENGTH: 2432
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-899

Query Match      4.1%; Score 114; DB 6; Length 2432;
Best Local Similarity 19.5%; Pred. No. 0.59;
Matches 89; Conservative 64; Mismatches 163; Indels 140; Gaps 20;

Qy 75 CLILQDDIPAPNIPSTDSHSSQLQNE-----QPSLATSSNOTSQD----- 117
Db 98 CUSVOTD-PTDEIPYKSKKKHKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 154
Qy 118 EQPSDS----FQQAQAQSGVWDDSMGLPSONFEAESIQDNAHMAEGTGYPSEPMLCSES 174
Db 155 DLESDSPFKDSEPSVALELPTRAFGPSEINSPAV-----VLEPPV--S 199
Qy 175 VEGQVPHSLFELYQADCSDDANDALIVLHLLMESGVIPOGTRAKALSMPEKWLKSGVY 234
Db 200 MEVSEPHILETLKPAKTAE-----LSVVSTSVISQSEQSVAVMPE-----PSMT 245
Qy 235 KLOYMHPCLCEGSSATLTCVPLGNLIVVNATLKNINRSVKRLQLLPESFICKE-----KL 290
Db 246 KILDSFAAPVPTTLVLKSEPVVTVMSVEYQMSVLKSVESSTPEPSKIMLVPPVAKV 305
Qy 291 GENVANYIKDLQKLSRLFKDLQVYPLLAFTR-----QALNLPDVFGLVVLPLELKLRFPL 346
Db 306 LEPSETLVVSSETTEVYPEPSTSTWDFPSSAIEALRLPE-----QP 349
Qy 347 LDVRSVLKSLAVCRDLFTASNDPLMLRFLYLRDRFRNTVRVQDQWKLKRYKRIHQKES 406
Db 350 VDVPEISADSSMTRP-----QEL-----PEL 370
Qy 407 PKGRFVMLPSSHTIPYPNPLHPRPPSSRLPGIIGGYDQRPYVGDPISSLIP 466
Db 371 PKTALQLQSSVASAMELPG-----PATSM-----BLQGPVPTPVLE-----LP 412
Qy 467 GPGETPSQFPPL-RPRFDPVGLPGPN-----PILPG 497
Db 413 GPSATP--VPPLPGPLSTPVELPGPATAVPELPG 446

RESULT 12
US-10-821-234-962
; Sequence 962, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 962
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; LENGTH: 791
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-962

Query Match      4.0%; Score 109.5; DB 6; Length 791;
Best Local Similarity 20.8%; Pred. No. 0.29;
Matches 80; Conservative 56; Mismatches 139; Indels 109; Gaps 17;

Qy 17 PETE-----PTLGHLSRLSLILCTGWTGYSNTR--FTITLN-----YKDPIT 57
Db 399 PEVESLPVASSSTLLPLAPSNSTSLNSTFGSTNLTGLFFPQLNGTANDTAGPELPDPLG 458
Qy 58 G-----DEETLASYGIVSGDLICLIQLDDIPAPNIPSPSTDSEHS-SLQNEQP-SLAT 108
Db 459 GLLDEAMLDEISLMDLAIEG-----FNPVQASQLEEEFSDSGLSDSSHSPSSLS 511
Qy 109 SSNQTSMDQEPSDSFQQAQAQSGVWDDSMGLPSONFEAESIQDNAHMAEG-TGTFYPS 167
Db 512 SEGSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 567
Qy 168 PMLCSEVEGOVPHSLFTL-----YQSADCSDDANDALIVLHLLMESGYIP-- 214
Db 568 SKFCRMSTY--QDPAQLSCLPYLEHVHGNHTYNNMAPSA-----LDSADLPPP 611
Qy 215 ---QGTEAKALSMPKWLKSGVYKLOYMHPCLCEGSSATLTCVPLGNLIVVNATLKNNE 270
Db 612 SALKKGSKKQADFLDKQMSRDEHARAMK-----IPTNDKIINLPVEEFNE 659
Qy 271 IRSVKRLQLLPESFI-----CKEKLGNVANYIKDLQKLSRLFKDLQVYP 315
Db 660 LLSKYQLSEAGLSLIRDRRRGNKMAAQNCRKRLDTILNLRDVEDLQR-DKARLLRE 718
Qy 316 LLAFTROALNL-----PDVEG 331
Db 719 KVEFLRSLRQMKQKQVQSLYQEVFG 742

RESULT 13
US-11-036-256-27
; Sequence 27, Application US/11036256
; Publication No. US20060026719A1
; GENERAL INFORMATION:
; APPLICANT: KIELISZEWSKI, MARCIA
; APPLICANT: XU, JIANFENG
; TITLE OF INVENTION: METHODS OF PRODUCING PEPTIDES/PROTEINS IN PLANTS AND
; TITLE OF INVENTION: PEPTIDES/PROTEINS PRODUCED THEREBY
; FILE REFERENCE: 27211/04130
; CURRENT APPLICATION NUMBER: US/11/036,256
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/602,562
; PRIOR FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/582,027
; PRIOR FILING DATE: 2004-06-22
; PRIOR APPLICATION NUMBER: 60/536,486
; PRIOR FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 27
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: amino acid construct
US-11-036-256-27

Query Match      3.9%; Score 106.5; DB 7; Length 200;
Best Local Similarity 29.3%; Pred. No. 0.073;
Matches 34; Conservative 7; Mismatches 46; Indels 29; Gaps 4;

Qy 414 LFPSTHTTIPFPNP-----LHPRPPSSRLPPGIIGGYDQRPYVGDPISSLIPG 467
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Db 34 LTPLPAPTPPLLPHPGTPPLTTLPLPAPTP-----PLLPHPGTPLTTLPL 79
QY 458 PGETSQPPPLPRDFVGPPLPGPN-PILPGRGGNDRF-----PFRPSGRP 514
Db 80 PAPTPLLPHPGTPPLTTLPLPAPTPLLPHPGTPPLTTLPLPAPTPLLPHPGTP 135

RESULT 14
US-11-036-256-31
; Sequence 31, Application US/11036256
; Publication No. US20060026719A1
; GENERAL INFORMATION:
; APPLICANT: KIELISZEWSKI, MARCIA
; APPLICANT: XU, JIANFENG
; TITLE OF INVENTION: METHODS OF PRODUCING PEPTIDES/PROTEINS IN PLANTS AND
; FILE REFERENCE: 27211/04130
; CURRENT APPLICATION NUMBER: US/11/036,256
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/502,562
; PRIOR FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/582,027
; PRIOR FILING DATE: 2004-06-22
; PRIOR APPLICATION NUMBER: 60/536,486
; PRIOR FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 31
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: amino acid construct
US-11-036-256-31

Query Match 3.9%; Score 106.5; DB 7; Length 228;
Best Local Similarity 33.7%; Pred. No. 0.088; Mismatches 6; Indels 25; Gaps 4;
Matches 35; Conservative 6; Mismatches 38; Indels 25; Gaps 4;
QY 414 LLPSSHTIPFYFN---PLHPRPPFSSRLPPGIIGGYDQRPYL-----PYV 457
Db 128 LSPSTPTPPGPHSPPPPLSPSPPTPL-----GPHSPPTLSPSTPTPPGVPVS 181
QY 458 GDPISLLIPGGETSQPPPLPRDFVGPPLPGPNPIL---PGR 498
Db 182 GTPLPTLPLPAPTPLLPHPGTPPLTTLPLPAPTPLLPHPGR 225

RESULT 15
US-11-150-845-10
; Sequence 10, Application US/11150845
; Publication No. US20060003399A1
; GENERAL INFORMATION:
; APPLICANT: Cytokinetics, Inc.
; APPLICANT: Tomasevic, Nenad
; APPLICANT: Jia, Zhiheng
; APPLICANT: Sakowicz, Roman
; APPLICANT: Pierce, Daniel
; APPLICANT: Finer, Jeffrey
; TITLE OF INVENTION: HIGH THROUGHPUT ACTIN POLYMERIZATION ASSAY
; FILE REFERENCE: 020552-007720US
; CURRENT APPLICATION NUMBER: US/11/150,845
; CURRENT FILING DATE: 2005-06-10
; PRIOR APPLICATION NUMBER: 60/673,444
; PRIOR FILING DATE: 2005-04-20
; PRIOR APPLICATION NUMBER: 60/578,949
; PRIOR FILING DATE: 2004-06-10
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 398
; TYPE: PRT

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(398)
; OTHER INFORMATION: 105WASP
US-11-150-845-10
Query Match 3.8%; Score 105; DB 7; Length 398;
Best Local Similarity 27.3%; Pred. No. 0.26; Mismatches 17; Indels 62; Gaps 10;
Matches 51; Conservative 17; Mismatches 57; Indels 62; Gaps 10;
QY 348 DVRSVLSLSAVCR-DLFTASNDPLLRFLYLDRDNTVRVQTDWKELYRKRHIQRKES 406
Db 162 DLRSLSFSGAGISEAQLTDAETSKLIYD-----IEDQGLEAVR-QEMRRQE- 207
QY 407 PKGRFVMLLSPSSTHTIPYPNPLHPRPFP---SRLP-PGIIGGYDQRPYLV----- 457
Db 208 -----PLPPPPPPSRGNQLPRPPIVGNKGRSGPLPPVPLGIA 246
QY 458 -----GDPISLLIPGGETSQPPPLPRDFVGPPLPGPNPILPGRGGNDRPFRPS 510
Db 247 PPPPTPRGPP-----PPGRGGPP-----PPPPPATGRSGPLPPPP-----PGAGGPPMPPPPPPP 296
QY 511 RGRPTDG 517
Db 297 PPPSSG 303
Search completed: February 14, 2006, 21:16:49
Job time : 19 secs